

Query Match 100.0%; Score 1237; DB 6; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1, 4e-84;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIAADRGAGGLPAAAGDHGIRGSKRRRHEVEQPEYDCGRDEPDRDFYPGEARPEPRP 60
 Best Local Similarity 100.0%; Pred. No. 1, 4e-84;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 404 AIAADRGAGGLPAAAGDHGIRGSKRRRHEVEQPEYDCGRDEPDRDFYPGEARPEPRP 463
 Qy 61 VDSRRAARQASGPHEITITALVGAVTSLOQELAHMRTHAPYCPYPPVYHHPHADTT 120
 Db 464 VDSRRAARQASGPHEITITALVGAVTSLOQELAHMRTHAPYCPYPPVYHHPHADTT 523
 Qy 121 PAQPRYPAKAVILPPHIAAPPGLSGAVPPSYPPVAVTPGAPPLHQPSPAHHPPP 180
 Db 524 PAQPRYPAKAVILPPHIAAPPGLSGAVPPSYPPVAVTPGAPPLHQPSPAHHPPP 583
 Qy 181 PPPGTPPPAASLFOPEAFGAEGALVNASSAAHVNVNTDARAAD 224
 Db 584 PPPGTPPPAASLFOPEAFGAEGALVNASSAAHVNVNTDARAAD 627

Qy 181 PPPGTPPPAASLFOPEAFGAEGALVNASSAAHVNVNTDARAAD 224
 Db 216 PAQPRYPAKAVILPPHIAAPPGLSGAVPPSYPPVAVTPGAPPLHQPSPAHHPPP 275

Qy 276 PPPGTPPPAASLFOPEAFGAEGALVNASSAAHVNVNTDARAAD 319

RESULT 2
 ID AAE36428 standard; protein; 637 AA.
 XX DT 07-AUG-2003 (first entry)
 XX DE HSV-2 UL26 full-length antigen.
 XX KW Herpes simplex virus; HSV; infection; vaccine; therapy; UL26; antigen.
 XX OS Herpes simplex virus type 2.
 XX OS Herpes simplex virus type 2.
 XX PN WO2003020108-A2.
 XX PD 13-MAR-2003.
 XX PR 27-AUG-2002; 2002WO-US027341.
 XX PR 04-SEP-2001; 2001US-0317159P.
 XX PR 17-APR-2002; 2002US-0373429P.
 XX PI (CORI-) CORIXA CORP.
 XX PI Hosken NA, Day CH;
 XX DR; 2003-290135/28.
 XX DR-N-PSDB; AAD55178.

Novel isolated polypeptide comprising immunogenic portion of a herpes simplex virus antigen, useful for detecting herpes simplex virus infection in a subject, and for treating the virus infection in a patient.

Claim 1: Page 110-112; 114pp; English.

The invention relates to polypeptides comprising an immunogenic portion of herpes simplex virus (HSV) antigen and to nucleic acid molecules encoding polypeptides. Polypeptides of the invention are useful for detecting and treating HSV infection in a patient. Polynucleotides of the invention are useful as diagnostic reagents for detecting HSV infection in a patient and also as a probes or primers. The invention is used to prepare vaccines. The present sequence is HSV-2 strain HG52 UL26 full-length antigen.

Sequence 637 AA;

Query Match 100.0%; Score 1237; DB 8; Length 637;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-84;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIAADRGAGGLPAAAGDHGIRGSKRRRHEVEQPEYDCGRDEPDRDFYPGEARPEPRP 60

4044	ATAADRGQQGULPAAAGDHGTRGSAKRREHEVEQPEYDCGRDDEPDRDFPPGEARPEPRP	463	Qy	121 PAQPRYPAKAVYLPPHIAAPPGLISGAVPPSPPPVATPGPAPLHQSPPAHPPP 180
671	VDSRRAARQASGPHEITITALVAVTSLSQQLAHMRTHAPGYPVPGYHADTE 120		Db	218 PAQPRYPAKAVYLPPHIAAPPGLISGAVPPSPPPVATPGPAPLHQSPPAHPPP 277
4644	VDSRRAARQASGPHEITITALVAVTSLSQQLAHMRTHAPGYPVPGYHADTE 523		Qy	181 PPPGPTPPPAASLPLPEPEAGAEAGALVNASSAAHYNVDTARAAD 224
			Db	278 PPPGPTPPPAASLPLPEPEAGAEAGALVNASSAAHYNVDTARAAD 321
				RESULT 5
				AAR64767
				ID AAR64767 standard; protein; 636 AA.
				XX AAR64767;
				AC AAR64767;
				XX 25-MAR-2003 (revised)
				DT 19-JUL-1995 (first entry)
				XX HSV-2 protease, ICP25.
				XX Protease; HSV-2; protease-inhibitor; virucide; ICP35.
				XX Herpes simplex virus type 2.
				OS WO9429456-A2.
				XX 22-DEC-1994.
				XX 25-MAY-1994; 94WO-US005920.
				PF 08-JUN-1993; 93US-00073819.
				PR 23-MAY-1994; 94US-00243390.
				XX (ABBO) ABBOTT LAB.
				XX Steffy KR, Kati WM, Katz L, Mcgonigal TP, Sarthy AV, Schoen SE;
				XX WPI: 1995-036483/05.
				XX N-PSDB; AAQ76261.
				XX New Herpes Simplex Virus type 2 protease - used in screening methods for identifying potential herpes viral protease inhibitor cpds.
				XX Claim 4; Fig 1A-1C; 56pp; English.
				XX HSV-2 DNA (given in AAQ76252) was isolated from Vero cells infected with HSV-2 strain Ci. The translated amino acid sequence is given in AA64767.
				CC The DNA was digested with BamHI, seqd. by gel electrophoresis and transferred to nitrocellulose. A nick-translated probe deriv. from HSV-1 protease was used for hybridization to identify DNA (AAQ76261) encoding HSV-2 protease (AAR64768) and the protease substrate ICP35 (AAR64769). (Updated on 25-MAR-2003 to correct PN field.)
				XX Sequence 636 AA;
				Query Match 99.7%; Score 1233; DB 2; Length 636;
				Best Local Similarity 99.6%; P-req. No. 2.7e-84; Indels 0; Gaps 0; Matches 223; Conservative 1; Mismatches 1; Mismatches 0; Indels 0; Gaps 0
				CC 1 AIAADRGQGLPAAAGDGIIGSAKRRHEVEPYEYDGGREDDDFPYPGGEARPEPRP 60
				Db 403 AIAADRGQGLPAAAGDGIIGSAKRRHEVEPYEYDGGREDDDFPYPGGEARPEPRP 462
				Qy 61 VDSRRAARQASGPHEITITALVAVTSLSQQLAHMRTHAPGYPVPGYHADTE 124
				Db 463 VDSRRAARQASGPHEITITALVAVTSLSQQLAHMRTHAPGYPVPGYHADTE 525
				Qy 121 PAQPRYPAKAVYLPPHIAAPPGLISGAVPPSPPPVATPGPAPLHQSPPAHPPP 180
				Db 523 PAQPRYPAAVYLPPHIAAPPGLISGAVPPSPPPVATPGPAPLHQSPPAHPPP 582
				Qy 181 PPPGPTPPPAASLPLPEPEAGAEAGALVNASSAAHYNVDTARAAD 224
				Db 158 VDSRRAARQASGPHEITITALVAVTSLSQQLAHMRTHAPGYPVPGYHADTE 217

Db 583 PPPGPTPPAASLPOPEAAGALVNASSAAHVNVDTARAAD 626

RESULT 6

AAR71017
ID AAR71017 standard; protein; 638 AA.
XX AAR71017;XX DT 25-MAR-2003 (revised)
XX 02-OCT-1995 (first entry)

XX HSV-2 protease.

XX Herpes simplex virus; HSV-2; capsid; UL26 gene.
OS Herpes simplex virus type 2.
XX WO9506055-A1.XX PD 02-MAR-1995.
XX PF 19-AUG-1994; 94WO-US009303.XX PR 20-AUG-1993; 93US-00110522.
XX 23-JUN-1994; 94US-00264537.

XX XX PA (SMITHKLINE BEECHAM CORP.

XX PI Dilella AG, Debouck CM;

XX XX PS WPI:1995-106803/14.
DR N-PSDB; AAQ84947.

XX New herpes simplex virus (HSV)-2 protease and capsid protein - used to develop prods. for use in the diagnosis and treatment of HSV-2 infections.

XX Claim 1; Fig 1; 51PP; English.

CC The sequence is the product of the herpes simplex virus type 2 gene UL26, which is the HSV-2 protease. The protein can be used in the diagnosis and treatment of HSV-2 infections. See also AAR71010-31. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 638 AA;

Query Match 99.7%; Score 1233; DB 2; Length 638;

Best Local Similarity 99.6%; Pred. No. 5.2e-84; Mismatches 1; Indels 0; Gaps 0; Matches 223; Conservative 1;

Db 1 AIAADRGQGLPAAAGDHGSAKRRHEVEQPYDCCRDEPRDFPYPPGEARPEPP 60

Db 405 AIAADRGQGLPAAAGDHGSAKRRHEVEQPYDCCRDEPRDFPYPPGEARPEPP 464

Db 61 VDSRRAAARQASGPHEITITALVGAITSLOQELAHRTHAPYGPYPYHPHADTE 120

Db 465 VDSRRAAARQASGPHEITITALVGAITSLOQELAHRTHAPYGPYPYHPHADTE 524

Db 121 PAQPRYPAKAVYLPPPHIAPPGPPPLSGAVPPPSYPPVATPGPAPPLHQPSPAHAHPP 180

Db 525 PAQPRYPAEAVYLPPPHIAPPGPPPLSGAVPPPSYPPVATPGPAPPLHQPSPAHAHPP 584

Db 181 PPPGPTPPAASLPOPEAAGALVNASSAAHVNVDTARAAD 224

Db 585 PPPGPTPPAASLQPOPEAAGALVNASSAAHVNVDTARAAD 628

RESULT 8

AAW72049

AAW72124 standard; protein; 642 AA.
XX DT 07-DEC-1998 (first entry)

AC AAW72124;

XX DT 18-DEC-1998 (first entry)

XX XX HSV-2 strain SB5 Contig ID 15 ORF#11 protein.

XX XX HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.

XX XX Herpes simplex virus 2.

XX XX WO920016-A1.

XX PN 09-DEC-1998.

XX PD 14-MAY-1998.

XX XX 97WO-US020016.

XX XX 96US-00310279P.

XX PR 09-JUN-1997; 97US-0049018P.

XX XX (SMITHKLINE BEECHAM CORP.

PA PA

XX PI Esser KM, Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB;

XX PI Leary JJ;

XX DR WPI; 1998-286847/25.

XX DR N-PSDB; AAV62159.

XX PT Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in mammal.

XX PS Claim 10; Page 92; 748pp; English.

XX XX This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 15. Based on homology, this sequence is a UL26 protein. The protein can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the protein can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.

XX SQ Sequence 642 AA;

Query Match 99.7%; Score 1233; DB 2; Length 642;

Best Local Similarity 99.6%; Pred. No. 5.2e-84;

Matches 223; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AIAADRGQGLPAAAGDHGSAKRRHEVEQPYDCCRDEPRDFPYPPGEARPEPP 60

Db 409 AIAADRGQGLPAAAGDHGSAKRRHEVEQPYDCCRDEPRDFPYPPGEARPEPP 468

QY 61 VDSRRAAARQASGPHEITITALVGAITSLOQELAHRTHAPYGPYPYHPHADTE 120

Db 469 VDSRRAAARQASGPHEITITALVGAITSLOQELAHRTHAPYGPYPYHPHADTE 528

QY 121 PAQPRYPAKAVYLPPPHIAPPGPPPLSGAVPPPSYPPVATPGPAPPLHQPSPAHAHPP 180

Db 529 PAQPRYPAEAVYLPPPHIAPPGPPPLSGAVPPPSYPPVATPGPAPPLHQPSPAHAHPP 588

QY 181 PPPGPTPPAASLPOPEAAGALVNASSAAHVNVDTARAAD 224

Db 589 PPPGPTPPAASLQPOPEAAGALVNASSAAHVNVDTARAAD 632

RESULT 8

AAW72049 standard; protein; 252 AA.

XX ID AAW72049;

XX AC AAW72124;

XX DT 07-DEC-1998 (first entry)

XX XX

DB HSV-2 strain SB5 Contig ID 104 ORF#17 protein.
 XX HSV-2 strain SB5; immunological response induction; therapy;
 KW antiviral identification; viral protein inhibitor.
 XX Herpes simplex virus 2.
 XX antiviral identification; viral protein inhibitor.
 OS Herpes simplex virus 2.
 XX OS Herpes simplex virus 2.
 PN WO9820016-A1.
 XX
 PD 14-MAY-1998.
 XX 97WO-US020016.
 PP 31-OCT-1997; 97WO-US020016.
 XX 04-NOV-1996; 96US-0030279P.
 PR 09-JUN-1997; 97US-0049018P.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX WPI: Chan JY, Dabrowski -Amaral CB, Delvecchio AM, Dillon SB;
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA Esser KM, Chan JY, Dabrowski -Amaral CE, Delvecchio AM, Dillon SB;
 PI Leary JJ;
 XX DR WPI: 1998-286847/25.
 DR N-PSDB; AAV62136.
 XX PT Herpes simplex virus type-2 sequences - useful in, e.g. prevention and
 PT treatment of infection or inducing immunological response in mammal.
 XX
 PS Claim 10; Page 58-59; 748pp; English.
 XX This sequence represents a Herpes simplex virus type-2 (HSV-2) protein
 CC sequence of the invention. This sequence was isolated from a HSV-2 strain
 CC sequence of the invention. This sequence was isolated from a HSV-2 strain
 CC deposited as ARCC VR-2546) DNA fragment designated Contig ID 104.
 CC Based on homology, this sequence is a Ul26 protease. The proteins can be
 CC used for the treatment or prevention of disease, to induce an
 CC immunological response in a mammal or to identify inhibitors, activators
 CC or novel antivirals. Antagonists of the proteins can be used to inhibit a
 CC viral polypeptide. The DNA sequence or a vector containing it can also be
 CC used to induce an immunological response in a mammal.
 XX Sequence 252 AA;
 SQ Sequence Match 99.3%; Score 1228; DB 2; Length 252;
 Best Local Similarity 99.1%; Pred. No. 5e-84; Indels 1; Gaps 0;
 Matches 222; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AIAADROQGLPAAAGDGIRESACKRHEVEQPEYDGRDPPYPPGEARPPRPRP 60
 Qy 1.9 AIAADROQGLPAAAGDGIRESACKRHEVEQPEYDGRDPPYPPGEARPPR 78
 Db 61 VDSRRAAFQASGPHETITALGVATSLQELAHMRATHAPGYPYHPHADET 120
 Qy 79 VDSRRAAFQASGPHETITALGVATSLQELAHMRATHAPGYPYHPHADET 138
 Db 121 PAQPRYPAKAYLPPPHIAPGPPLGAVPPSYPPVAYTGPAPLHQPSPAHAPP 180
 Qy 139 PAQPRYPAEAVYLPPPHIAPGPPLGAVPPSYPPVAVTGPAPLHQPSPAHAPP 198
 Db 181 PPPGPTPPPAASLPPQEAQGAEGALVNAASSAHV 215
 Qy 199 PPPGPTPPPAASLPPQEAQGAEGALVNAASSAHV 224
 *Db 199 PPPGPTPPPAASLPPQEAQGAEGALVNAASSAHV 242
 RESULT 10
 ID AAR71031 Standard; protein; 635 AA.
 XX
 AC AAR71031;
 XX
 AC AAR71031;
 DT 25-MAR-2003 (revised)
 XX DT 02-OCT-1995 (first entry)
 XX HSV-1 UL26 gene product.
 DE HSV-1 UL26 gene product.
 XX HSV-2 strain SB5; immunological response induction; therapy;
 KW HSV-2 strain SB5; immunological response induction; therapy;
 KW antiviral identification; viral protein inhibitor.

RESULT 9
 AAW72192
 ID AAW72192 standard; protein; 657 AA.
 XX
 AC AAW72192;
 XX
 DT 13-JAN-1999 (first entry)
 XX HSV-2 strain SB5 Contig ID 15 ORF#27 protein.
 DE HSV-2 strain SB5; immunological response induction; therapy;
 KW HSV-2 strain SB5; immunological response induction; therapy;

XX	UL26 protease deletion mutant D, amino acids 1-220 deleted.	DE	UL26 protease deletion mutant FF, amino acids 1-32 deleted.
XX	UL26; open reading frame; ORF; protease; herpes simplex virus; HSV; capsid protein; ICP35 c; ICP35 d; ICP35 e; ICP35 f; functional domain; insertion; deletion; substitution.	KW	KW; open reading frame; ORF; protease; herpes Simplex virus; HSV; capsid protein; ICP35; ICP35 c; ICP35 d; ICP35 e; ICP35 f; functional domain; insertion; deletion; substitution.
XX	OS	KW	KW
XX	Herpes simplex virus type 1.	KW	KW
XX	PN	OS	OS
XX	BP514830-A2.	PN	Herpes simplex virus type 1.
XX	XX	PN	PN
PD	25-NOV-1992.	PD	EP514830-A2.
XX	19-MAY-1992;	92EP-00108420.	XX
XX	PR 24-MAY-1991;	91US-00705814.	XX
PR 07-FEB-1992;	92US-00832855.	PR 24-MAY-1991;	91US-00705814.
XX	(ARCH-) ARCH DEV CORP.	XX	PR 07-FEB-1992;
PA	XX	PA	92US-00832855.
PI	Roizman B, Liu F;	PI	(ARCH-) ARCH DEV CORP.
XX	WPI; 1992-391444/48.	XX	PA
DR	DR	XX	XX
XX	New herpes serine proteases and corresp. nucleic acid sequences - for detection, prevention and treatment of infection caused by HSV, Epstein-Barr, Varicella-Zoster and CMV cytomealo-virus.	PT	New herpes serine proteases and corresp. nucleic acid sequences - for detection, prevention and treatment of infection caused by HSV, Epstein-Barr, Varicella-Zoster and CMV cytomealo-virus.
PT	PT	PT	PT
XX	XX	XX	XX
PS	PS	PS	PS
PS	Table 1; 66pp; English.	PS	Table 1; 66pp; English.
XX	XX	XX	XX
XX	The sequences given in AAR28635-52 are mutants of the protease encoded by the UL26 open reading frame (ORF). The UL26 ORF is contained within a section of the herpes simplex virus (HSV) type 1 genome for the family of HSV capsid proteins designated ICP35. The UL26 transcription initiation site is used as the start point for measurements of distance in this section of the genome. The UL26 protease and ICP35 precursor proteins, ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c and d gives ICP35 e and f respectively. Cleavage specificity of the UL26 protease is altered by the inclusion of these mutations. These mutations include insertions, deletions or substitutions which affect the functional domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)	The sequences given in AAR28635-52 are mutants of the protease encoded by the UL26 open reading frame (ORF). The UL26 ORF is contained within a section of the herpes simplex virus (HSV) type 1 genome for the family of HSV capsid proteins designated ICP35. The UL26 transcription initiation site is used as the start point for measurements of distance in this section of the genome. The UL26 protease and ICP35 precursor proteins, ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c and d gives ICP35 e and f respectively. Cleavage specificity of the UL26 protease is altered by the inclusion of these mutations. These mutations include insertions, deletions or substitutions which affect the functional domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)	
XX	XX	XX	XX
PS	PS	PS	PS
PS	Disclosure; Table 1; 66pp; English.	PS	Disclosure; Table 1; 66pp; English.
XX	XX	XX	XX
XX	The sequences given in AAR28635-52 are mutants of the protease encoded by the UL26 open reading frame (ORF). The UL26 ORF is contained within a section of the herpes simplex virus (HSV) type 1 genome for the family of HSV capsid proteins designated ICP35. The UL26 transcription initiation site is used as the start point for measurements of distance in this section of the genome. The UL26 protease and ICP35 precursor proteins, ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c and d gives ICP35 e and f respectively. Cleavage specificity of the UL26 protease is altered by the inclusion of these mutations. These mutations include insertions, deletions or substitutions which affect the functional domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)	The sequences given in AAR28635-52 are mutants of the protease encoded by the UL26 open reading frame (ORF). The UL26 ORF is contained within a section of the herpes simplex virus (HSV) type 1 genome for the family of HSV capsid proteins designated ICP35. The UL26 transcription initiation site is used as the start point for measurements of distance in this section of the genome. The UL26 protease and ICP35 precursor proteins, ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c and d gives ICP35 e and f respectively. Cleavage specificity of the UL26 protease is altered by the inclusion of these mutations. These mutations include insertions, deletions or substitutions which affect the functional domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)	
XX	XX	XX	XX
SQ	Sequence 415 AA;	SQ	Sequence 603 AA;
XX	XX	XX	XX
XX	Query Match 53.9%; Score 666.5; DB 2; Length 615;	XX	Query Match 53.9%; Score 666.5; DB 2; Length 603;
Best Local Similarity 63.0%; Pred. No. 7.5e-42;	Best Local Similarity 63.0%; Pred. No. 1.1e-41;	Best Local Similarity 63.0%; Pred. No. 1.1e-41;	Best Local Similarity 63.0%; Pred. No. 1.1e-41;
Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;	Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;	Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;	Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;
Qy 1 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 60	Qy 1 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 60	Qy 1 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 60	Qy 1 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 60
Db 183 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 241	Db 183 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 241	Db 371 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 429	Db 371 AIAADROAGGLPAAAGDGHGSGAKRERRHEVQEPEYDCGRDDEPDRDFPPYPGEARPEPRP 429
Qy 61 VDSRRAARQASQPHETITALVGAVTSIQQELAHMRARTHAPYGPYPPVGPYPPVGHPHADTE- 119	Qy 61 VDSRRAARQASQPHETITALVGAVTSIQQELAHMRARTHAPYGPYPPVGPYPPVGHPHADTE- 119	Qy 61 VDSRRAARQASQPHETITALVGAVTSIQQELAHMRARTHAPYGPYPPVGPYPPVGHPHADTE- 119	Qy 61 VDSRRAARQASQPHETITALVGAVTSIQQELAHMRARTHAPYGPYPPVGPYPPVGHPHADTE- 119
Db 242 VDSRRAARHSPGTNETITALGCAVTSIQQELAHMRARTSAPYGMVTPVAVHTRPQVGEPEP 301	Db 242 VDSRRAARHSPGTNETITALGCAVTSIQQELAHMRARTSAPYGMVTPVAVHTRPQVGEPEP 301	Db 430 VDSRRAARHSPGTNETITALGAVTSIQQELAHMRARTSAPYGMVTPVAVHTRPQVGEPEP 489	Db 430 VDSRRAARHSPGTNETITALGAVTSIQQELAHMRARTSAPYGMVTPVAVHTRPQVGEPEP 489
Qy 120 TPAQPPRXPYKAVYLPPPHIAPPPLHOPSPAH 177	Qy 120 TPAQPPRXPYKAVYLPPPHIAPPPLHOPSPAH 177	Qy 120 TPAQPPRXPYKAVYLPPPHIAPPPLHOPSPAH 177	Qy 120 TPAQPPRXPYKAVYLPPPHIAPPPLHOPSPAH 177
Db 302 TTTHPALCPPEAVYRPPHSAYGPPQOPPSHAPTPYAPACPPGPPP---PCPSTQT 358	Db 302 TTTHPALCPPEAVYRPPHSAYGPPQOPPSHAPTPYAPACPPGPPP---PCPSTQT 358	Db 490 TTTHPALCPPEAVYRPPHSAYGPPQOPPSHAPTPYAPACPPGPPP---PCPSTQT 546	Db 490 TTTHPALCPPEAVYRPPHSAYGPPQOPPSHAPTPYAPACPPGPPP---PCPSTQT 546
Qy 178 PPPPPPPTPPPAAASLQPQEAGAALVNASSAAHVNTDTARAAD 224	Qy 178 PPPPPPPTPPPAAASLQPQEAGAALVNASSAAHVNTDTARAAD 224	Qy 178 PPPPPPPTPPPAAASLQPQEAGAALVNASSAAHVNTDTARAAD 224	Qy 178 PPPPPPPTPPPAAASLQPQEAGAALVNASSAAHVNTDTARAAD 224
Db 359 RAPLPTBEPFPPATGSPEASNAEAGLVNASSAAHVNTDTARAAD 405	Db 359 RAPLPTBEPFPPATGSPEASNAEAGLVNASSAAHVNTDTARAAD 405	Db 547 RAPLPTBEPFPPATGSPEASNAEAGLVNASSAAHVNTDTARAAD 593	Db 547 RAPLPTBEPFPPATGSPEASNAEAGLVNASSAAHVNTDTARAAD 593
XX	XX	XX	XX
RESULT 13	RESULT 14	RESULT 15	RESULT 16
AAR28641	AAR28640	AAR28641	AAR28640
ID AAR28641 standard; protein; 603 AA.	ID AAR28640 standard; protein; 626 AA.	ID AAR28641 standard; protein; 603 AA.	ID AAR28640 standard; protein; 626 AA.
XX	XX	XX	XX
AC	AC	AC	AC
XX	XX	XX	XX
DT 25-MAR-2003 (revised)	DT 25-MAR-2003 (revised)	DT 24-MAR-1993 (first entry)	DT 24-MAR-1993 (first entry)

XX	UL26 protease deletion mutant EE, amino acids 1-9 deleted.
DE	
KW	UL26; open reading frame; ORF; protease; herpes simplex virus; HSV;
KW	capsid protein; ICP35; ICP35 c; ICP35 d; ICP35 e; ICP35 f;
TW	functional domain; insertion; deletion; substitution.
KW	
XX	
OS	Herpes simplex virus type 1.
XX	
PN	EP514830-A2.
XX	
PD	25-NOV-1992.
XX	
PP	19-MAY-1992; 92EP-00108420.
XX	
PR	24-MAY-1991; 91US-00705814.
XX	
PR	07-FEB-1992; 92US-0082855.
XX	
PPA	(ARCH-) ARCH DEV CORP.
XX	
PPI	Roizman B, Liu F;
XX	
DDR	WPI; 1992-391444/48.
XX	
PPT	New herpes serine proteases and correesp. nucleic acid sequences - for
PPT	detection, prevention and treatment of infection caused by HSV, Epstein-
PPT	Barr, Varicella-Zoster and CMV cytomegalovirus.
XX	
PS	Disclosure; Table 1; 66pp; English.
XX	
CCC	The sequences given in AAR28635-52 are mutants of the protease encoded
CCC	the UL26 open reading frame (ORF). The UL26 ORF is contained within a
CCC	section of the herpes simplex virus (HSV) type 1 genome for the family
CCC	HSV capsid proteins designated ICP35. The UL26 transcription initiation
CCC	site is used as the start point for measurements of distance in this
CCC	section of the genome. The UL26 protease and ICP35 precursor proteins,
CCC	ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35
CCC	and d gives ICP35 e and f respectively. Cleavage specificity of the UL
CCC	protease is altered by the inclusion of these mutations. These mutations
CCC	include insertions, deletions or substitutions which affect the function
CCC	domains of the protease. (Updated on 25-MAR-2003 to correct PN file.)

Sequence 626 AA;						
Query	Match	53.9%	Score 666.5;	DB 2;	Length 626;	
Best Local	Similarity	63.0%	pred. No. 1.1e-41;			
Matches	143;	Conservative	Mismatches 12;	Indels 7;	Gaps	
Qy	1	AIAADRGAGLPAAGDGHGIRGSAKRRHEVEQPYEDCGRDDEPDQDPYYPGEARPEPRP				
Qy	394	AIAADRGAGCQP-AAGDPGTRGSGRRYYAEGPSSYCDQDEPDADYYPGEARGAQPG				
Qy	61	VDSRRAARQASGPBETITALVAGNTSLSQQLAHMARTAPYCGYPYCPGYHHPHADTE-				
Qy	453	VDSRRAARISGPBETITALMAGNTSLSQQLAHMARTASAPGYHPTVAYHRQPGVEPPP				
Qy	120	TAQPPRYPAKAVYLPPLHIAPPGPLS - GAVPPPSYPVAVTPGPAPPHQSPSAAH				
Qy	513	TTTHPALCPEAVYRPYPHISAPYGPQGPQPSHAPYPPYPAACPGPPPP-- -PCPSTQ				
Qy	178	PPPPPPGPTPPAAASLQPQPEAAGALVNSASSAAHVNVDARAAD 224				
Qy	570	PPPPPPGPTPPAAASLQPQPEAAGALVNSASSAAHVNVDARAAD 224				

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XX UL26 protease.
 DE XX
 KW UL26; open reading frame; ORF; protease; herpes simplex virus; HSV;
 KW capsid protein; ICP35; ICP35 c; ICP35 d; ICP35 e; ICP35 f;
 KW functional domain.
 XX
 OS Herpes simplex virus type 1.
 XX EP514830-A2.
 XX PD 25-INQV-1992.
 XX PF 19-MAY-1992; 92EP-00108420.
 XX PR 24-MAY-1991; 91US-00705814.
 PR 07-FEB-1992; 92US-00832855.
 XX PA (ARCH-) ARCH DEV CORP.
 XX PI Roizman B, Liu F;
 XX DR 1992-391444/48.
 DR N-PSDB; AAQ30736.
 XX PT New herpes serine proteases and corresp. nucleic acid sequences - for
 PT detection, prevention and treatment of infection caused by HSV, Epstein-
 Barr, Varicella-Zoster and CMV cytomegalovirus.
 PT XX Disclosure; Fig 1B; 66pp; English.
 PS XX
 CC This sequence is encoded by the UL26 open reading frame (ORF) and it is a
 CC protease. The UL26 ORF is contained within a section of the herpes
 CC simplex virus (HSV) type 1 genome for the family of HSV capsid proteins
 CC designated ICP25. The UL26 transcription initiation site is used as the
 CC start point for measurements of distance in this section of the genome.
 CC The UL26 protease and ICP35 precursor proteins, ICP35 c and d, may be
 CC cleared by the UL26 protease. Cleavage of ICP35 c and d gives ICP35 e and
 CC f respectively. Cleavage specificity of the UL26 protease may be altered
 CC by mutations within the sequence. These mutations may be insertions or
 CC deletions or substitutions which affect the functional domains of the
 CC protease. See also AAR28635-52. (Updated on 25-MAR-2003 to correct PN

CC	XX	Sequence 635 AA;	Query Match	53 9%;	Score 666 5;	DB 2;	Length 635;
SQ			Best Local Matches	63 0%;	Pred. No. 1.1e-41;		
Qy	1	AIADDQAGGLPAAAGDGHGRGSAAKRRRHEVEPPYDCGRDDEPDPYYPGEARPEPRP	60	143	Conservative	53 matches	Length 635;
Db	403	AIADDQAGGQP-AAGDPGVGRSGCRRYEAGPSSYCDQEPDADYPYYPGEARAPRG	461				
Qy	61	VDSRAARHQSGPHETITIALGVATSLQQLAHMARTAAGPYPVGPVYHHPADTE-	119				
Db	462	VDSRAARHQSGPTNITIALMGAVTSQQLAHMARTASAGMVTVAHYRPQVGEPEP	521				
Qy	120	TPAQPPRYPKAVYIPLPPHIAAPPGLPLS - GAVPPPSYPPVATGPAPLHOPSAPAH	177				
Db	522	TTTHALCPPEAVTPPHSAFPYGAACPPGPPPPP--PCPSTQRT	578				
Qy	178	PPPPPGPTPPPAALPQPPAAGALVNASSIAHVNDTARAD	224				
Db	579	PPPPPGPTPPPAALPQPPAAGALVNASSIAHVNDTARAD	625				

Search completed: July 27, 2005, 12:18:38
Job time: 157 sec
233 KEEFIEFARFFAIGUE BROWNE

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 27, 2005, 12:31:33 ; Search time 39 Seconds

Title: US-10-623-429-9_COPY_475_483
Perfect score: 48
Sequence: 1 GPHEITAL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 1000 summaries

Database : PIR 79;*
1: PIR1;*
2: PIR2;*
3: PIR3;*
4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	79.2	83	2 S24712	Ig alpha chain - h
2	37	77.1	404	2 T35421	probable regulator
3	36	75.0	459	2 B86726	cell division prot
4	36	75.0	1825	2 C88400	protein H19w2.1
5	36	75.0	1825	2 T32828	[hypothetical prote
6	35	72.9	201	2 A1205	hypothetical prote
7	35	72.9	334	2 AB0936	N-acetyl-gamma-glu
8	35	72.9	515	1 T06595	2-amino-4-hydroxy-
9	35	72.9	724	2 T11404	hypothetical prote
10	35	72.9	1239	1 VHWVEV	structural polypro
11	35	72.9	1240	1 VHWVEV	structural polyprotein
12	35	72.9	1241	2 S26373	genome polyprotein
13	35	72.9	1242	2 A56605	structural polypro
14	35	72.9	1242	2 S72350	structural polypro
15	35	72.9	1324	2 T14073	peptide synthetase
16	34	70.8	143	2 A70573	hypothetical prote
17	34	70.8	478	2 T40860	probable alpha-amy
18	34	70.8	653	2 G82971	probable ferredoxi
19	33	68.8	181	2 D87196	probable membrane
20	33	68.8	259	2 C70530	hypothetical prote
21	33	68.8	384	2 AD0049	hypothetical prote
22	33	68.8	418	2 B69014	hypothetical prote
23	33	68.8	511	2 D69675	phosphoglycerate m
24	33	68.8	557	2 E86106	yida protein f simi
25	33	68.8	557	2 S56342	yida protein - Esc
26	33	68.8	557	2 H91265	hypothetical prote
27	33	68.8	613	2 D87380	hypothetical prote
28	33	68.8	633	2 S49788	probable membrane
29	33	68.8	635	1 WMBEN6	capaid protein - h

30	33	68.8	706	2 DB2452	anaerobic ribonucl
31	33	68.8	707	1 A6047	ribonucleoside-tri
32	33	68.8	712	1 A47331	ribonucleoside-tri
33	33	68.8	712	2 AC1058	anaerobic ribonucl
34	33	68.8	712	2 G91280	anaerobic ribonucl
35	33	68.8	712	2 G86121	ribonucleoside-tri
36	33	68.8	712	2 AG0419	probable membrane
37	33	68.8	971	1 S55495	major surface glyc
38	33	68.8	1008	2 T30544	major surface glyc
39	33	68.8	1017	2 T30542	serine hydroxymeth
40	33	68.8	1022	2 T30543	Glycine hydroxymet
41	33	68.8	1179	2 C36793	probable lipid tra
42	33	68.8	1267	1 MNXR31	hypothetical prote
43	33	68.8	1267	1 MNXR32	lambda 3 protein -
44	33	68.8	1267	1 MNXR33	lambda 3 protein -
45	32.5	67.7	467	2 T38353	serine hydroxymeth
46	32.5	67.7	472	2 T37218	Glycine hydroxymet
47	32.5	67.7	479	1 A42241	probable lipid tra
48	32	66.7	118	2 T02042	lipid transfer pro
49	32	66.7	118	2 T03300	probable lipid tra
50	32	66.7	118	2 H75583	probable copper re
51	32	66.7	141	2 B69199	hypothetical prote
52	32	66.7	168	2 C70507	hypothetical prote
53	32	66.7	179	2 C90435	hypothetical prote
54	32	66.7	343	2 B83851	N-acyl-L-amino aci
55	32	66.7	404	2 B98012	cell division prot
56	32	66.7	425	2 D95444	hypothetical prote
57	32	66.7	429	2 D95444	nicotinam acetylch
58	32	66.7	466	2 PC4296	hypothetical prote
59	32	66.7	479	2 D70841	flagellar hook-ass
60	32	66.7	554	2 T08976	hypothetical prote
61	32	66.7	579	2 B44857	peptide synthet
62	32	66.7	680	2 T03106	probable transport
63	32	66.7	680	2 T08080	probable myrosinas
64	32	66.7	858	2 E72419	two-component syst
65	32	66.7	912	2 T18785	hypothetical prote
66	32	66.7	1213	2 T37559	yersinibactin bio
67	32	66.7	2015	2 AC0233	probable polyketid
68	32	66.7	2035	2 A48854	L-serine ammonia
69	32	66.7	2041	2 T17439	hypothetical prote
70	31	64.6	29	2 S34762	two-component syst
71	31	64.6	98	2 D95571	T-cell receptor be
72	31	64.6	132	2 G82805	hypothetical prote
73	31	64.6	139	2 S03485	hypothetical prote
74	31	64.6	201	2 T24183	hypothetical prote
75	31	64.6	261	2 C84366	carbamate kinase (
76	31	64.6	315	2 H86336	fatty acid/phospho
77	31	64.6	327	2 T44433	uroporphyrinogen d
78	31	64.6	339	2 B71918	uroporphyrinogen d
79	31	64.6	340	2 D64595	opein, pineal glan
80	31	64.6	351	1 A55962	N-acyl-L-amino aci
81	31	64.6	370	2 JG6130	paired box transcr
82	31	64.6	370	2 F69233	carbamoyl-phosphat
83	31	64.6	374	2 D83618	beta-ketoacyl-Co
84	31	64.6	401	2 AG1323	threonine dehydrat
85	31	64.6	422	2 AH1694	threonine dehydrat
86	31	64.6	422	2 T19748	VI polyphosphate (
87	31	64.6	434	2 JC2545	polymyxin B resist
88	31	64.6	434	2 I36802	excision repair pr
89	31	64.6	435	2 T35884	quinate-shikimate
90	31	64.6	455	2 B70654	probable membrane
91	31	64.6	521	2 S55317	alpha-D-mannosidas
92	31	64.6	558	2 JC5799	hypothetical prote
93	31	64.6	583	1 S55609	p53-binding protei
94	31	64.6	668	2 S22660	hypothetical prote
95	31	64.6	772	2 T35884	Rag-1 protein - ch
96	31	64.6	809	2 A55547	Rag-1 protein - ch
97	31	64.6	964	2 S4804	Rag-1 protein - ch
98	31	64.6	1018	2 JC5799	Rag-1 protein - ch
99	31	64.6	1027	2 T35878	Rag-1 protein - ch
100	31	64.6	1039	2 S42519	RAG-1 protein - ch
101	31	64.6	1041	2 S42511	RAG-1 protein - ch

103	3.1	64.6	1043	2	B33754	gene tramtrack-p88
104	3.1	64.6	1043	2	A31754	periodic trypthophan
105	3.1	64.6	1045	2	I51555	hypothetical protein
106	3.1	64.6	1087	2	F7283	recombination acti
107	3.1	64.6	1231	2	S51089	beta-galactosidase
108	3.1	64.6	1254	2	T18277	protein-tyrosine-p
109	3.1	64.6	1488	2	T02856	kinase heavy chain
110	3.1	64.6	1762	2	T03222	probable membrane
111	3.1	64.6	15281	2	S41309	probable polypeptide
112	30.5	63.5	274	2	AB4302	cyclic coprin synthase
113	3.0	62.5	25	2	S22221	ketopantoate hydroperoxidase (EC 1.1.1.1)
114	3.0	62.5	49	2	T07309	hypothetical protein
115	3.0	62.5	114	2	E97017	hypothetical protein
116	3.0	62.5	126	2	C90797	hypothetical protein
117	3.0	62.5	148	2	EB7609	hypothetical protein
118	3.0	62.5	196	2	T10206	ketopantoate hydroperoxidase (EC 1.1.1.1)
119	3.0	62.5	210	2	D72490	hypothetical protein
120	3.0	62.5	281	2	B84337	deoxyribose-phosphate
121	3.0	62.5	225	2	F86417	hypothetical protein
122	3.0	62.5	245	2	H97865	pseudouridylate synthase (kanamycin kinase)
123	3.0	62.5	262	1	P885K	probable integral membrane protein
124	3.0	62.5	269	2	DB4001	hypothetical protein
125	3.0	62.5	269	2	GB1230	conserved hypothetical protein
126	3.0	62.5	281	2	T5932	probable inositol
127	3.0	62.5	283	2	T15229	hypothetical protein
128	3.0	62.5	286	2	T25559	hypothetical protein
129	3.0	62.5	291	2	S79602	peroxidase (EC 1.1.1.1)
130	3.0	62.5	296	2	T12469	hypothetical protein
131	3.0	62.5	301	2	T37326	probable transcript
132	3.0	62.5	313	2	EB7705	hypothetical protein
133	3.0	62.5	319	2	H62806	divalent cation transporter
134	3.0	62.5	331	2	C97493	malonyl-CoA-acyl C
135	3.0	62.5	331	2	AB2711	malonyl-CoA:acyl C
136	3.0	62.5	334	1	RDCBP	N-acetyl-gamma-glu
137	3.0	62.5	334	2	G91239	N-acetyl-gamma-glu
138	3.0	62.5	334	2	DB6087	SRP family of GTP-
139	3.0	62.5	351	2	DB5930	hypothetical protein
140	3.0	62.5	360	2	C82220	peroxidase (EC 1.1.1.1)
141	3.0	62.5	363	2	S31780	phospholipase D
142	3.0	62.5	364	2	E81702	hypothetical protein
143	3.0	62.5	371	2	D85606	probable integral membrane protein
144	3.0	62.5	389	2	C9776	probable flagellar
145	3.0	62.5	393	2	AG0991	nitrogenase cofactor
146	3.0	62.5	395	2	B47071	O-antigen ligase I
147	3.0	62.5	404	2	AB0973	O-antigen ligase II
148	3.0	62.5	404	2	B41317	hypothetical protein
149	3.0	62.5	405	2	T40193	probable integrase
150	3.0	62.5	409	2	F90825	hypothetical protein
151	3.0	62.5	413	2	T48089	probable integrase
152	3.0	62.5	416	2	AB684	glutathione-disulfide
153	3.0	62.5	454	2	A82353	hypothetical protein
154	3.0	62.5	483	2	S75369	galactose-1-phosphatase
155	3.0	62.5	493	2	C9216	UTP-Nhexose-1-phosphatase
156	3.0	62.5	530	1	A36080	galactose-1-phosphatase
157	3.0	62.5	532	2	D97264	mannuronan C-5-epi
158	3.0	62.5	497	2	S77785	oligo-1,6-glucosidase
159	3.0	62.5	508	2	B83788	hypothetical protein
160	3.0	62.5	517	2	T05620	glycine hydroxymethyl
161	3.0	62.5	518	1	S42118	probable fatty acyl
162	3.0	62.5	530	1	A46690	transactivator EBN
163	3.0	62.5	532	2	T01759	glycine hydroxymethyl
164	3.0	62.5	553	2	S77623	mannuronan C-5-epi
165	3.0	62.5	561	2	GB4012	oligo-1,6-glucosidase
166	3.0	62.5	577	2	T18116	hypothetical protein
167	3.0	62.5	599	2	D72454	glycine hydroxymethyl
168	3.0	62.5	637	2	H7254	probable DNA gyrase
169	3.0	62.5	638	2	JCT753	ring finger B-box
170	3.0	62.5	640	2	F93364	hypothetical protein
171	3.0	62.5	642	2	S45452	probable membrane
172	3.0	62.5	648	1	D7BPS2	DNA-directed DNA
173	3.0	62.5	655	2	G7090	probable pria protein
174	3.0	62.5	718	2	A31342	penicillin-binding
175	3.0	62.5	739	1	VH1WEB	nucleocapsid protein

249	60.4	S76696	2	RRNZNV	1	2204
250	60.4	AC1142	2	S56274	29	60.4
251	60.4	AF1500	2	PR8 protein - yea	29	60.4
252	60.4	393	2	FAB1 protein - homoi	29	60.4
253	60.4	393	2	erythronolide synt	2403	2
254	60.4	394	2	6-deoxyerythronoli	2	T30875
255	60.4	405	2	surfactin syntheta	2	S22012
256	60.4	424	2	dynin gamma heavy	2	S13595
257	60.4	426	2	syringomycin synth	2	140485
258	60.4	426	2	hypothetical prote	2	T08044
259	60.4	441	2	tripeptidyl peptid	2	4485
260	60.4	449	2	MEG22 protein - hu	2	2
261	60.4	449	2	probable retrotrans	2	D84516
262	60.4	455	1	probable tagatose	2	T08044
263	60.4	455	1	probable tagatose	2	2
264	60.4	462	2	probable tagatose	2	AH1978
265	60.4	464	2	N-acyl-L-amino aci	2	2
266	60.4	468	2	hypothetical prote	2	2
267	60.4	487	2	conserved hypothet	2	2
268	60.4	487	2	interferon-related	2	2
269	60.4	491	2	interferon-related	2	2
270	60.4	491	2	phosphoprotein-related	2	2
271	60.4	491	2	phosphoprotein-related	2	2
272	60.4	491	2	phosphoprotein-related	2	2
273	60.4	491	2	phosphoprotein-related	2	2
274	60.4	508	2	phosphoprotein-related	2	2
275	60.4	513	2	cyclochrome P450 Cy	2	2
276	60.4	513	2	cyclochrome P450 Cy	2	2
277	60.4	521	2	cyclochrome P450 Cy	2	2
278	60.4	543	2	cyclochrome P450 Cy	2	2
279	60.4	556	2	cyclochrome P450 Cy	2	2
280	60.4	558	2	cyclochrome P450 Cy	2	2
281	60.4	568	2	cyclochrome P450 Cy	2	2
282	60.4	577	2	cyclochrome P450 Cy	2	2
283	60.4	590	2	cyclochrome P450 Cy	2	2
284	60.4	622	2	cyclochrome P450 Cy	2	2
285	60.4	624	2	cyclochrome P450 Cy	2	2
286	60.4	641	2	cyclochrome P450 Cy	2	2
287	60.4	651	2	cyclochrome P450 Cy	2	2
288	60.4	665	1	cyclochrome P450 Cy	2	2
289	60.4	684	2	cyclochrome P450 Cy	2	2
290	60.4	693	2	cyclochrome P450 Cy	2	2
291	60.4	700	2	cyclochrome P450 Cy	2	2
292	60.4	701	2	cyclochrome P450 Cy	2	2
293	60.4	733	2	cyclochrome P450 Cy	2	2
294	60.4	770	2	cyclochrome P450 Cy	2	2
295	60.4	776	2	cyclochrome P450 Cy	2	2
296	60.4	788	2	cyclochrome P450 Cy	2	2
297	60.4	867	2	cyclochrome P450 Cy	2	2
298	60.4	878	2	cyclochrome P450 Cy	2	2
299	60.4	980	2	cyclochrome P450 Cy	2	2
300	60.4	980	2	cyclochrome P450 Cy	2	2
301	60.4	1102	2	cyclochrome P450 Cy	2	2
302	60.4	1148	2	cyclochrome P450 Cy	2	2
303	60.4	1209	2	cyclochrome P450 Cy	2	2
304	60.4	1209	2	cyclochrome P450 Cy	2	2
305	60.4	1210	2	cyclochrome P450 Cy	2	2
306	60.4	1243	2	cyclochrome P450 Cy	2	2
307	60.4	1246	2	cyclochrome P450 Cy	2	2
308	60.4	1254	1	cyclochrome P450 Cy	2	2
309	60.4	1254	1	cyclochrome P450 Cy	2	2
310	60.4	1255	1	cyclochrome P450 Cy	2	2
311	60.4	1354	2	cyclochrome P450 Cy	2	2
312	60.4	1255	1	cyclochrome P450 Cy	2	2
313	60.4	1282	2	cyclochrome P450 Cy	2	2
314	60.4	1283	2	cyclochrome P450 Cy	2	2
315	60.4	1307	2	cyclochrome P450 Cy	2	2
316	60.4	1322	2	cyclochrome P450 Cy	2	2
317	60.4	1354	2	cyclochrome P450 Cy	2	2
318	60.4	1364	2	cyclochrome P450 Cy	2	2
319	60.4	1466	2	cyclochrome P450 Cy	2	2
320	60.4	1506	2	cyclochrome P450 Cy	2	2
321	60.4	1974	2	cyclochrome P450 Cy	2	2
322	60.4			hypothetical prote	2	2
323	60.4			N-acyl-L-amino aci	2	2
324	60.4			hypothetical prote	2	2
325	60.4			conserved hypothet	2	2
326	60.4			interferon-related	2	2
327	60.4			probable lipid met	2	2
328	60.4			probable tagatose	2	2
329	60.4			probable tagatose	2	2
330	60.4			probable tagatose	2	2
331	60.4			probable tagatose	2	2
332	60.4			probable tagatose	2	2
333	60.4			probable tagatose	2	2
334	60.4			probable tagatose	2	2
335	60.4			probable tagatose	2	2
336	60.4			probable tagatose	2	2
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354	60.4			probable tagatose	2	2
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356	60.4			probable tagatose	2	2
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363	60.4			probable tagatose	2	2
364	60.4			probable tagatose	2	2
365	60.4			probable tagatose	2	2
366	60.4			probable tagatose	2	2
367	60.4			probable tagatose	2	2
368	60.4			probable tagatose	2	2
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397	28	58.3	329	2	T0444	470	28	58.3	2	AB3040
398	28	58.3	329	2	T2221	471	28	58.3	2	D70782
399	28	58.3	332	2	F33600	472	28	58.3	2	B98246
400	28	58.3	332	2	G75344	473	28	58.3	2	T47554
401	28	58.3	335	2	JC1441	474	28	58.3	2	T36714
402	28	58.3	340	2	H83805	475	28	58.3	2	E70687
403	28	58.3	341	2	S09913	476	28	58.3	2	S76101
404	28	58.3	345	2	B5274	477	28	58.3	2	F69215
405	28	58.3	349	2	T23308	478	28	58.3	2	AC3373
406	28	58.3	351	2	AP2844	479	28	58.3	2	T31964
407	28	58.3	351	2	H97621	480	28	58.3	2	AB1022
408	28	58.3	353	2	H84332	481	28	58.3	2	A40656
409	28	58.3	353	2	A95398	482	28	58.3	2	G1BPSV
410	28	58.3	358	2	H6408	483	28	58.3	2	S76949
411	28	58.3	359	2	B96505	484	28	58.3	2	T26843
412	28	58.3	369	2	A89777	485	28	58.3	2	G85046
413	28	58.3	373	2	H72756	486	28	58.3	2	A70755
414	28	58.3	374	2	T2513	487	28	58.3	2	B70503
415	28	58.3	375	2	A80306	488	28	58.3	2	B76939
416	28	58.3	375	2	H71121	489	28	58.3	2	AB3343
417	28	58.3	377	2	F71877	490	28	58.3	2	T26843
418	28	58.3	382	2	T28691	491	28	58.3	2	F71877
419	28	58.3	384	2	A22257	492	28	58.3	2	AF3100
420	28	58.3	388	2	D5496	493	28	58.3	2	T39740
421	28	58.3	388	2	S41940	494	28	58.3	2	T01121
422	28	58.3	388	2	H71121	495	28	58.3	2	72K mitochondrial
423	28	58.3	388	2	A10208	496	28	58.3	2	hypothetical prote
424	28	58.3	391	1	TVBBI	497	28	58.3	2	adenine deaminase
425	28	58.3	392	2	T8133	498	28	58.3	2	adenine deaminase
426	28	58.3	395	2	AB1977	499	28	58.3	2	hypothetical prote
427	28	58.3	396	2	A75345	500	28	58.3	2	probable amylase
428	28	58.3	399	2	D5279	501	28	58.3	2	DNA topoisomerase
429	28	58.3	399	2	A83556	502	28	58.3	2	cyanobacteriophage
430	28	58.3	400	2	T31152	503	28	58.3	2	cucumisin (EC 3.4.2.1)
431	28	58.3	402	2	H65599	504	28	58.3	2	0.7K alpha-transferrin
432	28	58.3	402	2	E71912	505	28	58.3	2	probable aldehyde
433	28	58.3	404	2	JC5784	506	28	58.3	2	zinc finger, C3HC4
434	28	58.3	407	2	S29841	507	28	58.3	2	0.7K alpha-transferrin
435	28	58.3	408	2	G9100	508	28	58.3	2	trans-acting transcription factor
436	28	58.3	408	2	E97968	509	28	58.3	2	cation-transporter
437	28	58.3	408	2	AD3237	510	28	58.3	2	hypothetical prote
438	28	58.3	416	2	F72723	511	28	58.3	2	hypothetical prote
439	28	58.3	416	2	S76858	512	28	58.3	2	vesicle protein so
440	28	58.3	419	2	A85864	513	28	58.3	2	hypothetical prote
441	28	58.3	419	2	G91019	514	28	58.3	2	sensor protein tor
442	28	58.3	419	2	S56073	515	28	58.3	2	hypothetical prote
443	28	58.3	422	2	H82236	516	28	58.3	2	N-methyl-D-aspartate
444	28	58.3	422	2	A98306	517	28	58.3	2	probable ABC-type
445	28	58.3	423	2	T36467	518	28	58.3	2	major tegumental
446	28	58.3	425	1	JH0710	519	28	58.3	2	hypothetical prote
447	28	58.3	428	2	I51087	520	28	58.3	2	integrin alpha-4-c
448	28	58.3	430	2	D73382	521	28	58.3	2	lysine-keratulata
449	28	58.3	433	2	C83271	522	28	58.3	2	hypothetical prote
450	28	58.3	434	2	E81139	523	28	58.3	2	protein-tyrosine k
451	28	58.3	440	2	C83368	524	28	58.3	2	protein-tyrosine k
452	28	58.3	445	2	AD962	525	28	58.3	2	protein-tyrosine k
453	28	58.3	449	2	H70526	526	28	58.3	2	protein-tyrosine k
454	28	58.3	450	2	B69198	527	28	58.3	2	hypothetical prote
455	28	58.3	456	2	AF0093	528	28	58.3	2	protein-tyrosine k
456	28	58.3	458	2	E7244	529	28	58.3	2	protein-tyrosine k
457	28	58.3	461	2	I61080	530	28	58.3	2	protein-tyrosine k
458	28	58.3	465	1	DEBY4	531	28	58.3	1	protein-tyrosine k
459	28	58.3	465	2	F70364	532	28	58.3	1	protein-tyrosine k
460	28	58.3	467	2	T28848	533	28	58.3	1	hypothetical prote
461	28	58.3	467	2	D85583	534	28	58.3	1	protein-tyrosine k
462	28	58.3	467	2	E7240	535	28	58.3	1	protein-tyrosine k
463	28	58.3	467	2	B82225	536	28	58.3	1	protein dehydrogen
464	28	58.3	468	2	S39832	537	28	58.3	1	DNA-directed RNA P
465	28	58.3	469	2	S76919	538	28	58.3	1	DNA-directed RNA P
466	28	58.3	475	2	F85430	539	28	58.3	1	1-pyrroline-5-carb
467	28	58.3	480	2	G70678	540	28	58.3	2	AC3580

541	28	58.3	1224	2	T43218	Hi-transporting tw
542	28	58.3	1228	2	C98119	probable glutathio
543	28	58.3	1228	2	AG3067	hypothetical prote
544	28	58.3	1230	2	H84515	probable ring-hydr
545	28	58.3	124	2	E81779	hypothetical prote
546	28	58.3	125	2	T18556	heme d1 biosynthes
547	28	58.3	1303	2	C87519	core antigen - hep
548	28	58.3	1310	2	153597	hypothetical prote
549	28	58.3	1320	1	D64843	hypothetical prote
550	28	58.3	1320	1	S66279	protochlorophyll
551	28	58.3	1320	2	AB0633	hypothetical prote
552	28	58.3	1320	2	D90786	hypothetical prote
553	28	58.3	1320	2	B85646	probable sigma-70
554	28	58.3	1323	2	AH0225	hypothetical prote
555	28	58.3	1350	2	T30341	hypothetical prote
556	28	58.3	1386	2	T18334	transcription regu
563	28	58.3	1403	1	A41410	gibB protein - Pse
564	28	58.3	1535	2	S46224	olfactory receptor
565	28	58.3	1617	2	B86583	hypothetical prote
566	28	58.3	1636	2	B82736	hypothetical prote
567	28	58.3	1640	2	H88034	probable secreted
568	28	58.3	1715	2	G84429	ABC transporter [im
569	28	58.3	1848	2	A44140	chemotaxis protein
570	28	58.3	1896	2	T08851	transcription regu
571	28	58.3	1957	2	T38077	gibB protein - Pse
572	28	58.3	2052	2	F50515	olfactory receptor
573	28	58.3	2185	1	S60200	hypothetical prote
574	28	58.3	2261	2	T07084	hypothetical prote
575	28	58.3	2453	2	S60254	natural killer cel
576	28	58.3	2607	2	T31678	peroxidase - frui
577	27	57.3	3573	2	S23070	Down syndrome cell
578	28	58.3	3643	2	T36410	hypothetical prote
579	27	56.2	40	2	T31067	myosin X - bovine
580	27	56.2	5175	2	T20992	acetyl-CoA carboxy
581	27	56.2	5198	2	T43290	cellulose-binding
582	27	56.2	6713	2	B89921	Down syndrome cell
583	27	56.2	430	2	T28143	hypothetical prote
584	27	56.2	57.3	2	S23070	erythronolide synth
585	27	56.2	469	2	A87561	probable polyketid
586	27	56.2	40	2	S60200	BIR repeat contain
587	27	56.2	51	2	T37012	hypothetical prote
588	27	56.2	62	2	F81810	nuclear receptor c
589	27	56.2	65	2	F83727	bacitracin synthet
590	27	56.2	66	2	A87561	erythronolide synth
591	27	56.2	79	2	S31013	probable polyketid
592	27	56.2	94	2	H83655	BIR repeat contain
593	27	56.2	99	2	B97409	hypothetical prote
594	27	56.2	104	2	T23204	hemicitin precurs
595	27	56.2	107	2	T23204	hypothetical prote
596	27	56.2	108	1	CCWB	hypothetical prote
597	27	56.2	112	1	ASLJSX	hypothetical prote
598	27	56.2	113	1	E64695	hypothetical prote
599	27	56.2	116	2	AI0746	flagellar transcri
600	27	56.2	119	1	XMECBP	flagellar transcri
601	27	56.2	119	2	B90954	regulator of flaga
602	27	56.2	119	2	P85802	regulator of flaga
603	27	56.2	121	2	S59680	ribosomal protein
604	27	56.2	125	2	G71000	hypothetical prote
605	27	56.2	128	2	G97116	stress-induced pro
606	27	56.2	129	2	PC1254	endonuclease [BC
607	27	56.2	131	2	AD2648	conserved hypothet
608	27	56.2	133	2	T36638	probable substrate
609	27	56.2	137	1	C97430	hypothetical prote
610	27	56.2	138	2	AD2050	hypothetical prote
611	27	56.2	139	2	D82285	ferredoxin VC753
612	27	56.2	141	2	T49659	hypothetical prote
613	27	56.2	142	2	B70634	probable mmpS1 pro
614	27	56.2	144	2	E72705	hypothetical prote
615	27	56.2	145	2	T34303	leech antiplatelet
616	27	56.2	145	2	A42435	hypothetical prote
617	27	56.2	147	2	D70777	CBS domain protein
618	27	56.2	157	2	F87574	hypothetical prote
619	27	56.2	157	2	T27757	signal recognition
620	27	56.2	160	2	S45632	2-hydroxyconic s
621	27	56.2	161	2	T09807	probable ABC trans
622	27	56.2	161	2	C7641	high-affinity bran
623	27	56.2	166	2	G8384	probable thioester
624	27	56.2	166	2	T27705	probable thioester
625	27	56.2	172	2	F8581	probable thioester
626	27	56.2	174	2	S53149	probable thioester
627	27	56.2	183	2	T38917	probable thioester
628	27	56.2	190	2	E84060	probable thioester
629	27	56.2	191	2	B84472	probable thioester
630	27	56.2	191	2	S48826	probable thioester
631	27	56.2	201	2	B86488	probable thioester
632	27	56.2	203	2	D81236	probable thioester
633	27	56.2	206	2	B69121	probable thioester
634	27	56.2	208	2	T10337	probable thioester
635	27	56.2	224	1	RGE8BT	probable thioester
636	27	56.2	224	1	BWP8BP	probable thioester
637	27	56.2	228	2	T46559	probable thioester
638	27	56.2	229	2	T11104	probable thioester
639	27	56.2	229	2	G86524	probable thioester
640	27	56.2	229	2	D87221	probable thioester
641	27	56.2	239	2	B82123	probable thioester
642	27	56.2	239	2	S64573	probable thioester
643	27	56.2	239	2	A99291	probable thioester
644	27	56.2	240	2	AC2748	probable thioester
645	27	56.2	240	2	B97329	probable thioester
646	27	56.2	240	2	AB3357	probable thioester
647	27	56.2	242	2	E83738	probable thioester
648	27	56.2	244	2	T48110	probable thioester
649	27	56.2	245	2	A87485	probable thioester
650	27	56.2	245	2	D70670	probable thioester
651	27	56.2	248	2	S03688	probable thioester
652	27	56.2	248	2	E75302	probable thioester
653	27	56.2	249	2	E83738	probable thioester
654	27	56.2	253	2	E69098	probable thioester
655	27	56.2	253	2	S22763	probable thioester
656	27	56.2	254	2	T29704	probable thioester
657	27	56.2	254	2	T02078	probable thioester
658	27	56.2	256	2	JS02813	probable thioester
659	27	56.2	256	2	B82076	probable thioester
660	27	56.2	257	2	G84712	probable thioester
661	27	56.2	258	1	F270X2	probable thioester
662	27	56.2	258	2	E87615	probable thioester
663	27	56.2	258	2	JS07711	probable thioester
664	27	56.2	259	2	D84343	probable thioester
665	27	56.2	259	2	JC5271	probable thioester
666	27	56.2	260	2	S10016	probable thioester
667	27	56.2	261	2	A83727	probable thioester
668	27	56.2	261	2	T35168	probable thioester
669	27	56.2	266	2	E85775	probable thioester
670	27	56.2	266	2	C47127	probable thioester
671	27	56.2	267	2	H90233	probable thioester
672	27	56.2	273	2	D84195	probable thioester
673	27	56.2	273	2	G87037	probable thioester
674	27	56.2	274	2	AF3291	probable thioester
675	27	56.2	274	2	A89715	probable thioester
676	27	56.2	274	2	T44344	probable thioester
677	27	56.2	274	2	C7144	probable thioester
678	27	56.2	274	2	S10073	probable thioester
679	27	56.2	274	2	F81583	probable thioester
680	27	56.2	274	2	E85775	probable thioester
681	27	56.2	274	2	F81729	probable thioester
682	27	56.2	274	2	E87541	probable thioester
683	27	56.2	274	2	E87541	probable thioester
684	27	56.2	274	2	E87541	probable thioester
685	27	56.2	274	2	E87541	probable thioester
686	27	56.2	274	2	E87541	probable thioester

687	27	286	2	B70833	760	27	56.2	2	B26470
688	27	286	2	B9615	761	27	56.2	2	AH0908
689	27	287	2	A81803	762	27	56.2	2	C75040
690	27	287	2	DB1065	763	27	56.2	2	A91142
691	27	287	2	C97453	764	27	56.2	2	B65115
692	27	287	2	A26671	765	27	56.2	2	D85987
693	27	287	2	H75512	766	27	56.2	2	B86625
694	27	287	2	A36051	767	27	56.2	2	T30306
695	27	287	2	G27293	768	27	56.2	2	G72638
696	27	287	2	AB1145	769	27	56.2	2	F97333
697	27	290	1	NDPBT	770	27	56.2	2	H86315
698	27	290	2	G88229	771	27	56.2	2	C84166
699	27	290	2	AB1106	772	27	56.2	2	T08264
700	27	290	2	F86749	773	27	56.2	2	S16275
701	27	290	2	T36030	774	27	56.2	2	C64764
702	27	290	2	AG3407	775	27	56.2	2	S70072
703	27	290	2	NDPBT	776	27	56.2	2	PD0007
704	27	290	2	T44955	777	27	56.2	2	JC5674
705	27	290	2	A25698	778	27	56.2	2	AF2422
706	27	290	2	A64449	779	27	56.2	2	B36807
707	27	290	2	G35631	780	27	56.2	2	AR2752
708	27	290	2	QQLX1	781	27	56.2	2	Cytochrome P450 no
709	27	290	2	B87112	782	27	56.2	2	unknown protein F9
710	27	290	2	T44955	783	27	56.2	2	hypothetical prote
711	27	290	2	A56650	784	27	56.2	2	N-acyl-L-amino aci
712	27	290	2	A36305	785	27	56.2	2	hypothetical prote
713	27	290	2	H70723	786	27	56.2	2	CT011 hypotethical
714	27	290	2	AG3407	787	27	56.2	2	signal recognition
715	27	290	2	QQLX1	788	27	56.2	2	probable transcript
716	27	290	2	B87112	789	27	56.2	2	probable signal re
717	27	290	2	H83851	790	27	56.2	2	hypothetical prote
718	27	290	2	T25459	791	27	56.2	2	conserved hypothet
719	27	290	2	H70723	792	27	56.2	2	ical
720	27	290	2	AG3407	793	27	56.2	2	hypothetical prote
721	27	290	2	QQLX1	794	27	56.2	2	conserved hypothet
722	27	290	2	B21102	795	27	56.2	2	ical
723	27	290	2	H81553	796	27	56.2	2	hypothetical prote
724	27	290	2	D85507	797	27	56.2	2	hypothetical prote
725	27	290	2	E72116	798	27	56.2	2	hypothetical prote
726	27	290	2	A44504	799	27	56.2	2	hypothetical prote
727	27	290	2	E70684	800	27	56.2	2	asparagine-tRNA S
728	27	290	2	A0963	801	27	56.2	2	asparagine-tRNA S
729	27	290	2	S61517	802	27	56.2	2	asparagine-tRNA S
730	27	290	2	A97445	803	27	56.2	2	asparagine-tRNA S
731	27	290	2	B86179	804	27	56.2	2	asparagine-tRNA S
732	27	290	2	E69031	805	27	56.2	2	asparagine-tRNA S
733	27	290	2	AH3016	806	27	56.2	2	asparagine-tRNA S
734	27	290	2	A9267	807	27	56.2	2	asparagine-tRNA S
735	27	290	2	A43383	808	27	56.2	2	asparagine-tRNA S
736	27	290	2	E84398	809	27	56.2	2	asparagine-tRNA S
737	27	290	2	A3586	810	27	56.2	2	asparagine-tRNA S
738	27	290	2	G62138	811	27	56.2	2	asparagine-tRNA S
739	27	290	2	AH514	812	27	56.2	2	asparagine-tRNA S
740	27	290	2	B87500	813	27	56.2	2	asparagine-tRNA S
741	27	290	2	T22065	814	27	56.2	2	asparagine-tRNA S
742	27	290	2	B87376	815	27	56.2	2	asparagine-tRNA S
743	27	290	2	T3717	816	27	56.2	2	asparagine-tRNA S
744	27	290	2	H87557	817	27	56.2	2	asparagine-tRNA S
745	27	290	2	AB0595	818	27	56.2	2	asparagine-tRNA S
746	27	290	2	AB0595	819	27	56.2	2	asparagine-tRNA S
747	27	290	2	AB0595	820	27	56.2	2	asparagine-tRNA S
748	27	290	2	AB0595	821	27	56.2	2	asparagine-tRNA S
749	27	290	2	AB0595	822	27	56.2	2	asparagine-tRNA S
750	27	290	2	AB0595	823	27	56.2	2	asparagine-tRNA S
751	27	290	2	AB0595	824	27	56.2	2	asparagine-tRNA S
752	27	290	2	AB0595	825	27	56.2	2	asparagine-tRNA S
753	27	290	2	AB0595	826	27	56.2	2	asparagine-tRNA S
754	27	290	2	AB0595	827	27	56.2	2	asparagine-tRNA S
755	27	290	2	AB0595	828	27	56.2	2	asparagine-tRNA S
756	27	290	2	AB0595	829	27	56.2	2	asparagine-tRNA S
757	27	290	2	AB0595	830	27	56.2	2	asparagine-tRNA S
758	27	290	2	AB0595	831	27	56.2	2	asparagine-tRNA S
759	27	290	2	AB0595	832	27	56.2	2	asparagine-tRNA S
687	27	286	2	B70833	760	27	56.2	2	carbon-monoxide de
688	27	286	2	B9615	761	27	56.2	2	probable carbonic
689	27	287	2	A81803	762	27	56.2	2	probable integral
690	27	287	2	DB1065	763	27	56.2	2	hypothetical prote
691	27	287	2	C97453	764	27	56.2	2	cytochrome C oxid
692	27	287	2	A26671	765	27	56.2	2	cytochrome C oxid
693	27	287	2	H75512	766	27	56.2	2	formanidopyrimidin
694	27	287	2	A36051	767	27	56.2	2	H+/K+ -exchanging A
695	27	287	2	G27293	768	27	56.2	2	phosphate butyryl
696	27	287	2	AB1145	769	27	56.2	2	hypothetical prote
697	27	290	1	NDPBT	770	27	56.2	2	exodeoxyribonuclea
698	27	290	2	G88229	771	27	56.2	2	ribonuclease (EC 2.7
699	27	290	2	AB1106	772	27	56.2	2	hypothetical prote
700	27	290	2	F86749	773	27	56.2	2	pseudouridine synth
701	27	290	2	T36030	774	27	56.2	2	probable Fructokin
702	27	290	2	AG3407	775	27	56.2	2	florinacol 1
703	27	290	2	NDPBT	776	27	56.2	2	resist
704	27	290	2	T44955	777	27	56.2	2	2-dehydro-3-deoxyg
705	27	290	2	A25698	778	27	56.2	2	ribonuclease (EC 2.7
706	27	290	2	A64449	779	27	56.2	2	probable protein k
707	27	290	2	G35631	780	27	56.2	2	formylmethanofuran
708	27	290	2	QQLX1	781	27	56.2	2	probable iron-chel
709	27	290	2	B87112	782	27	56.2	2	trans-activating t
710	27	290	2	T44955	783	27	56.2	2	conserved hypothet
711	27	290	2	A56650	784	27	56.2	2	probable mitochondrial
712	27	290	2	A36305	785	27	56.2	2	2-oxoglutarate car
713	27	290	2	H70723	786	27	56.2	2	boxylate mal
714	27	290	2	AG3407	787	27	56.2	2	hypothetical prote
715	27	290	2	QQLX1	788	27	56.2	2	Na+/K+-exchanging
716	27	290	2	B87112	789	27	56.2	2	sitB protein
717	27	290	2	H83851	790	27	56.2	2	probable transcript
718	27	290	2	T25459	791	27	56.2	2	hypothetical prote
719	27	290	2	H70723	792	27	56.2	2	hypothetical prote
720	27	290	2	AG3407	793	27	56.2	2	Na+/K+-exchanging
721	27	290	2	QQLX1	794	27	56.2	2	sitB protein
722	27	290	2	B21102	795	27	56.2	2	probable transcript
723	27	290	2	H81553	796	27	56.2	2	hypothetical prote
724	27	290	2	D85507	797	27	56.2	2	hypothetical prote
725	27	290	2	E72116	798	27	56.2	2	hypothetical prote
726	27	290	2	A44504	799	27	56.2	2	hypothetical prote
727	27	290	2	E70684	800	27	56.2	2	phospholipase A2-a
728	27	290	2	A0963	801	27	56.2	2	ficolin-1 precurso
729	27	290	2	S61517	802	27	56.2	2	hypothetical prote
730	27	290	2	A97445	803	27	56.2	2	hypothetical prote
731	27	290	2	B86179	804	27	56.2	2	conserved hypothet
732	27	290	2	E69031	805	27	56.2	2	fructose bisphosph
733	27	290	2	AH3016	806	27	56.2	2	hypothetical prote
734	27	290	2	A9267	807	27	56.2	2	phosphate ABC tran
735	27	290	2	A43383	808	27	56.2	2	phosphate ABC tran
736	27	290	2	E84398	809	27	56.2	2	hypothetical prote
737	27	290	2	A3586	810	27	56.2	2	hypothetical prote
738	27	290	2	G62138	811	27	56.2	2	hypothetical prote
739	27	290	2	AH514	812	27	56.2	2	hypothetical prote
740	27	290	2	B87500	813	27	56.2	2	hypothetical prote
741	27	290	2	T22065	814	27	56.2	2	probable 3'-(2',5'-
742	27	290	2	B87376	815	27	56.2	2	hypothetical prote
743	27	290	2	T3717	816	27	56.2	2	hypothetical prote
744	27	290	2	H87557	817	27	56.2	2	hypothetical prote
745	27	290	2	AB0595	818	27	56.2	2	hypothetical prote
746	27</								

833	27	B89787	906	27	56.2	802	2	F70600
834	27	509	907	27	56.2	803	2	JC5569
835	27	56.2	908	27	56.2	822	2	S6810
836	27	56.2	909	27	56.2	832	2	S7815
837	27	510	910	27	56.2	836	2	S54152
838	27	56.2	911	27	56.2	842	2	T04880
839	27	56.2	912	27	56.2	859	2	T35785
840	27	517	913	27	56.2	859	2	T05470
841	27	56.2	914	27	56.2	863	1	SHNC
842	27	523	915	27	56.2	876	2	T33176
843	27	532	916	27	56.2	879	2	T49796
844	27	533	922	27	56.2	879	2	AC2108
845	27	56.2	923	27	56.2	907	2	S51254
846	27	538	918	27	56.2	917	2	S26723
847	27	56.2	919	27	56.2	918	2	A56832
848	27	548	920	27	56.2	919	2	CB7445
849	27	533	921	27	56.2	901	2	AC0149
850	27	56.2	922	27	56.2	901	2	AC64101
851	27	552	923	27	56.2	879	2	S23199
852	27	553	924	27	56.2	917	2	G-utrophin - mouse
853	27	56.2	925	27	56.2	918	2	major surface protein - yeast
854	27	523	926	27	56.2	920	2	probable mmp17 pro
855	27	56.2	927	27	56.2	901	2	translocon -
856	27	56.2	928	27	56.2	901	2	conserved hypothet-
857	27	56.2	929	27	56.2	987	2	G-utrophin - mouse
858	27	56.2	930	27	56.2	987	2	probable membrane protein
859	27	558	931	27	56.2	1002	2	hypothetical prote
860	27	56.2	932	27	56.2	1046	2	Ferritinase (FC 1).
861	27	56.2	933	27	56.2	1059	1	S67786
862	27	56.2	934	27	56.2	966	2	S18555
863	27	56.2	935	27	56.2	987	2	endo-1,4-beta-D-xylo-
864	27	56.2	936	27	56.2	1076	2	probable DNA mismatch
865	27	56.2	937	27	56.2	1076	2	repair protein
866	27	56.2	938	27	56.2	1076	2	DNA mismatch repair
867	27	56.2	939	27	56.2	1063	2	hypothetical prote
868	27	56.2	940	27	56.2	1063	2	structural polypro
869	27	56.2	941	27	56.2	1063	2	hypothetical prote
870	27	56.2	942	27	56.2	1076	2	hypothetical prote
871	27	56.2	943	27	56.2	1076	2	hypothetical prote
872	27	56.2	944	27	56.2	1081	2	hypothetical prote
873	27	56.2	945	27	56.2	1121	2	hypothetical prote
874	27	56.2	946	27	56.2	1148	2	hypothetical prote
875	27	56.2	947	27	56.2	1199	2	hypothetical prote
876	27	56.2	948	27	56.2	1225	2	hypothetical prote
877	27	56.2	949	27	56.2	1225	2	multidrug resistance
878	27	56.2	950	27	56.2	1235	1	QQBEM4
879	27	56.2	951	27	56.2	1254	1	epidermal growth f-
880	27	56.2	952	27	56.2	1254	1	cell division prot
881	27	56.2	953	27	56.2	1289	2	cell division prot
882	27	56.2	954	27	56.2	1289	2	hypothetical prote
883	27	56.2	955	27	56.2	1302	2	hypothetical prote
884	27	56.2	956	27	56.2	1329	2	hypothetical prote
885	27	56.2	957	27	56.2	1330	1	GQFFPE
886	27	56.2	958	27	56.2	1342	1	E886174
887	27	56.2	959	27	56.2	1342	2	G90510
888	27	56.2	960	27	56.2	1342	2	T17242
889	27	56.2	961	27	56.2	1374	2	D72593
890	27	56.2	962	27	56.2	1385	2	A64228
891	27	56.2	963	27	56.2	1441	2	T25828
892	27	56.2	964	27	56.2	1441	2	T47141
893	27	56.2	965	27	56.2	1475	2	T02335
894	27	56.2	966	27	56.2	1533	2	S42718
895	27	56.2	967	27	56.2	1533	2	T21052
896	27	56.2	968	27	56.2	1533	2	F71274
897	27	56.2	969	27	56.2	1581	2	T3131
898	27	56.2	970	27	56.2	1681	2	S42659
899	27	56.2	971	27	56.2	1799	1	S28381
900	27	56.2	972	27	56.2	1822	2	T50307
901	27	56.2	973	27	56.2	1822	2	probable protein t-
902	27	56.2	974	27	56.2	1822	2	acyl-CoA carboxy-
903	27	56.2	975	27	56.2	1822	2	giant protein P619
904	27	56.2	976	27	56.2	1822	2	ryanodine receptor
905	27	56.2	977	27	56.2	1822	2	ryanodine receptor
			978	27	56.2	1822	2	ryanodine receptor

979 27 56.2 5037 2 B35041
 980 27 56.2 7463 2 T3248
 981 27 56.2 13055 2 T16580
 982 26.5 55.2 132 2 E86317
 983 26.5 55.2 132 2 F70654
 984 26.5 55.2 173 2 A72625
 985 26.5 55.2 332 2 D95373
 986 26.5 55.2 395 2 S76793
 987 26.5 55.2 439 2 B82114
 988 26.5 55.2 1186 2 S72229
 989 26.5 55.2 1205 2 T18517
 990 26.5 55.2 1292 2 T02229
 991 26 54.2 36 2 A63827
 992 26 54.2 56 2 A49619
 993 26 54.2 64 2 D99799
 994 26 54.2 64 2 GB8659
 995 26 54.2 77 2 B82441
 996 26 54.2 77 2 D89887
 997 26 54.2 84 2 S63410
 998 26 54.2 84 2 S63323
 999 26 54.2 84 2 D70967
 1000 26 54.2 92 2 C27733

ALIGNMENTS

RESULT 1
 S24712 Ig alpha chain - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C;Accession: S24712
 R;Trapsis, A.
 Submitted to the EMBL Data Library, August 1992

A;Reference number: S24708

A;Accession: S24712

A;Molecule type: mRNA

A;Residues: 1-83 <TS>

A;Cross-references: EMBL:214963; NID:928571; PIDN:CAA78686_1; PID:g28572

C;Keywords: immunoglobulin

Query Match Score 38%; DB 2; Length 83;
 Best Local Similarity 79.2%; Pred. No. 0 93%;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETTAL 9

Db 22 GPHETTPL 30

RESULT 2
 T35421 Probable regulatory protein - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C;Accession: T35421
 C;Oliver, K.; Harris, D.; Bentley, S.D.; Partillier, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A;Reference number: Z21577
 A;Accession: T35421
 A;Molecule type: DNA
 A;Residues: 1-104 <OLI>

A;Cross-references: UNIPROT:O9X7X6; EMBL:AL049485; PIDN:CA839714_1; GSPDB:GN00070; SCOED
 A;Experimental source: strain A3 (2)
 C;Genetics:
 A;Gene: SCOEDB:SC6A5_30C

Query Match Score 37%; DB 2; Length 404;
 Best Local Similarity 66.7%; Pred. No. 8.9%;
 Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 0;

Qy 1 GPHETTAL 9
 Db 296 GPHEATAAL 304

RESULT 3
 E86726 cell division protein FtsY [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C;Accession: E86726
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaiillon, O.; Malarrie, K.; Weissenbach, J.; Ehrlich
 Genome Res 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp.
 A;Reference number: A86625; MJD:21235186; PMID:11337471
 A;Accession: E86726
 A;Cross-references: UNIPROT:Q0CHB9; GB:AB005176; PIDN:AAK04911_1; GSPDB:G
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: ftsY
 C;Superfamily: cell division protein ftsY

Query Match Score 75.0%; DB 2; Length 459;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
 Db 374 PHETIAN 381

RESULT 4

C88400 protein H19M22_1 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: C88400
 C;Anonymous, The C. elegans Sequencing Consortium
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A;Reference number: A75000; MJD:99069513; PMID:99151916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: C88400
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9UB28; UNIPROT:Q9UB29; GB:chr_III; PIDN:AA894997_1; PID:9274
 C;Genetics:
 A;Gene: H19M22_1
 A;Map position: 3

Query Match Score 75.0%; DB 2; Length 1825;
 Best Local Similarity 77.8%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETTAL 9
 Db 288 GPHETTGL 296

RESULT 5
 T32828 hypothetical protein H19M22_1 - Caenorhabditis elegans (fragment)
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T32828
 R;Wilson, R.; Wamsley, P.
 submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid H19M22.

A;Reference number: Z21229

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-1825 <WIL>

A;Cross-references: UNIPROT:Q9UB29; UNIPROT:Q9UB29; EMBL:AF040648; PIDN:AAB94997.1; GSPD

A;Experimental source: strain Bristol N2; clone H19M22

C;Genetics:

A;Gene: CESP1H19M22.1

A;Map position: 3

A;Intron position: 271/8

Query Match Score 36; DB 2; Length 1825;
 Best Local Similarity 75.0%; Pred. No. 78; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 2;

Qy 1 GPHEIT 9
 Db 288 GPHFTITGL 296

RESULT 6

AI2205 hypothetical protein alr3200 [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AI2205
 A;Cross-references: UNIPROT:Q9UB29; EMBL:AF040648; PIDN:AAB94997.1; GSPD

A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: alr3200

Query Match Score 35; DB 2; Length 201;
 Best Local Similarity 71.4%; Pred. No. 11; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 0;

Qy 1 GPHEIT 7
 Db 38 GPHEITVS 44

RESULT 7

AB0936 N-acetyl-gamma-glutamyl-phosphate reductase [imported] - *Salmonella enterica* subsp. entericaA;Species: *Salmonella enterica* subsp. enterica serovar TyphiA;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0936
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar

A;Reference number: AB0502; MUID:11677608

A;Accession: AB0936

A;Molecule type: DNA

A;Residues: 1-334 <PAR>

A;Cross-references: GB:AU513382; PIDN:CAD09508.1; PIDN:916504625; GSPDB:GN00176

C;Genetics:

A;Gene: SRY3752

C;Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase

Query Match Score 35; DB 2; Length 334;
 Best Local Similarity 87.5%; Pred. No. 19; Indels 1; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 2 PHETIT 9
 Db 25 PHETIT 32

RESULT 8

T06595 2-amino-4-hydroxymethylidihydropteridine diphosphokinase (EC 2.7.6.3) - garden pea
 N;Contains: 2-amino-4-hydroxymethylidihydropteridine pyrophosphokinase (EC 2.7.6.3)

C;Species: *Pisum sativum* (Garden pea)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: T06595

A;Note: Parts of this sequence, including the amino end of the mature protein, were determined.

C;Function: <HPPK>
 A;Description: EC 2.7.6.3 [validated, MUID:97224122]
 A;Pathway: Folate biosynthesis

C;Function: <DHFS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status predicted <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

F;232-488/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status predicted <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: Folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthase protein; 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphotransferase; folate biosynthesis

C;Keywords: dihydropteridine diphosphotransferase; folate biosynthesis; mitochondrial

C;Function: bifunctional folic acid synthase protein #status experimental <TP>

F;29-515/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase

F;48-179/Domain: 2-amino-4-hydroxymethylidihydropteridine diphosphotransferase homology <DHS>

A;

C;Genetics:
A;Map position: 4COP9-4 G3845

Query Match 72.9%; Score 35; DB 2; Length 724;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHETITAL 9
Db 526 GPHENIASL 534

RESULT 10
VHWEE
structural polyprotein - eastern equine encephalomyelitis virus (strain 82v-2137)
N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein C;Species: eastern equine encephalomyelitis virus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A26816
R;Chang, G.J.J.; Trent, D.W.
J;Gen; Virol. 68, 2129-2142, 1987
A;Title: Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus
A;Reference number: A26816; MUID:87282265; PMID:2886548
A;Accession: A26816
A;Molecule type: mRNA
A;Residues: 1-1239 <CH1>
A;Cross-references: UNIPROT:PO8768; EMBL:X05816; PID:562074; PIDN:CAA29261.1; PID:962075
C;Superfamily: togavirus structural polyprotein
C;Keywords: coat protein; glycoprotein; transmembrane protein
F;1-259/Product: coat protein C #status predicted <CPC>
F;260-322/Product: membrane glycoprotein E3 #status predicted <MG3>
F;323-742/Product: membrane glycoprotein E2 #status predicted <MG2>
F;64-701/Domain: transmembrane #status predicted <TN1>
F;727-737/Domain: transmembrane #status predicted <TN2>
F;743-798/Product: 6K protein #status predicted <K6P>
F;777-798/Domain: transmembrane #status predicted <TN4>
F;1211-1235/Product: membrane glycoprotein E1 #status predicted <MG1>
F;49,270,624,637,932/Binding site: carbohydrate (Asn) (covalent) #status predicted <TN5>
P;49,270,624,637,932/Binding site: carbohydrate (Asn) (covalent) #status predicted <BP1>

Query Match 72.9%; Score 35; DB 1; Length 1239;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 289 PHETITML 296

RESULT 11
VHWEE
structural polyprotein - eastern equine encephalomyelitis virus (strain VA33 [Ten Broeck])
N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein C;Species: eastern equine encephalomyelitis virus
C;Accession: A39992
R;Weaver, S.C.; Scott, T.W.; Rico-Hesse, R.
Virology 182, 774-784, 1991
A;Title: Molecular evolution of eastern equine encephalomyelitis virus in North America.
A;Reference number: A39992; MUID:91220727; PMID:2024496
A;Accession: A39992
A;Molecule type: genomic RNA
A;Residues: 1-1240 <WEA>
A;Cross-references: UNIPROT:P27284; GB:ME69094; PID:9323696; PIDN:AAA42980.1; PID:9323697
A;Note: the authors translated the codon AGC for residue 836 as Arg and GGU for residue 837 as Cys
C;Superfamily: togavirus structural polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-260/Product: coat protein C #status predicted <CPC>
F;261-323/Product: membrane glycoprotein E3 #status predicted <TM1>
F;324-743/Product: membrane glycoprotein E2 #status predicted <EG2>
P;49,271,625,638,834,933/Binding site: carbohydrate (Asn) (covalent) #status predicted <TM5>

Query Match 72.9%; Score 35; DB 2; Length 1240;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 290 PHETITML 297

RESULT 12
S26373
VHWEE
structural polyprotein - eastern equine encephalomyelitis virus genome polyprotein - eastern equine encephalomyelitis virus
N;Contains: 6K protein; capsid protein C; envelope protein E1; envelope protein E2; envelope protein E3
C;Species: eastern equine encephalomyelitis virus
C;Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S26373
R;Voichkov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Mikrobiol. nukleotid. sekvence of the eastern equine encephalomyelitis virus genome
A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus genome
A;Reference number: S26369; MUID:91375524; PMID:1896061
A;Accession: S26373
A;Molecule type: mRNA
A;Residues: 1-1241 <EVOL>
A;Cross-references: UNIPROT:Q66579; EMBL:X63135; NID:959185; PIDN:CAA44845.1; PID:959186
A;Note: sequence could not be checked because of bad print in paper
C;Superfamily: togavirus structural polyprotein
C;Keywords: capsid protein; envelope protein; glycoprotein; polyprotein
F;1-260/Product: capsid protein; glycoprotein; polyprotein
F;261-323/Product: envelope protein E3 #status predicted <EG3>
F;324-743/Product: envelope protein E2 #status predicted <EG2>
F;744-800/Product: 6K protein #status predicted <6KP>
F;801-1244/Product: 6K protein #status predicted <BP1>
F;801-1244/Product: envelope protein E1 #status predicted <BP1>

Query Match 72.9%; Score 35; DB 2; Length 1241;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 290 PHETITML 297

RESULT 13
AS6605
VHWEE
structural polyprotein - eastern equine encephalomyelitis virus (strain 4789)
C;Species: eastern equine encephalomyelitis virus
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: AS6605
R;Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Calisher, C.H.
Arch. Virol. 127, 305-314, 1992
A;Title: Genetic characterization of an antigenic subtype of eastern equine encephalomyelitis virus
A;Reference number: A56605; MUID:33090093; PMID:1280945
A;Accession: AS6605
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-1240 <WEA>
A;Cross-references: UNIPROT:Q08359; GB:120951; PID:9405814; PIDN:AAA02897.1; PID:g305047
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:119924, NCBIPI:119931)
C;Superfamily: togavirus structural polyprotein
C;Keywords: polyprotein

Query Match 72.9%; Score 35; DB 2; Length 1242;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 291 PHETITAL 298

RESULT 14
S72350 structural polyprotein - eastern equine encephalomyelitis virus
N: Contains: 6K protein; capsid protein; E1 protein; E2 protein; E3 protein
C: Species: eastern equine encephalomyelitis virus
C: Date: 04-May-1998 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
C: Accession: S72350
R: Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.J.; Virology 197, 375-390, 1993
A: Title: A comparison of the nucleotide sequences of eastern and western equine encephalitis viruses
A: Reference number: S72349; MUID:94025587; PMID:8105605
A: Accession: S72350
A: Status: preliminary
A: Molecule type: genomic RNA
A: Residues: 1-1242 <W2R>
A: Cross-references: UNIPROT:Q88700; EMBL:101034; PIDN:9391006; PIDN: AAC533735.1; PID:93930
C: Superfamily: togavirus structural polyprotein

Query Match 72.9%; Score 35; DB 2; Length 1242;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 291 PHETITAL 298

RESULT 15
T14070 peptide synthetase - Streptomyces fradiae (fragment)
C: Species: Streptomyces fradiae
C: Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C: Accession: T14070
R: Hosted, T.J.; Baltz, R.H.
Submitted to the EMBL Data Library, July 1997
A: Reference number: Z17868
A: Accession: T14070
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-1324 <HOS>
A: Cross-references: UNIPROT:052048; EMBL:AF016696; PID:g2738764; PID:g2738765; PIDN: AAC0
C: Genetics:
A: Note: cps-1
C: Superfamily: Mycobacterium tuberculosis mbtE protein; acetate-CoA ligase homology; acyl
C: Keywords: carrier protein; phosphopantetheine; phosphoprotein
P; 188-642/Domain: acetate-CoA ligase homology <ACL>
P; 659-727/Domain: acyl carrier protein homology <ACP>
P; 631/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 72.9%; Score 35; DB 2; Length 1324;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPHETI 6
Db 659 GPHETI 664

RESULT 16
A70573 hypothetical protein Rv2626c - Mycobacterium tuberculosis (strain H37RV)
C: Species: Mycobacterium tuberculosis
C: Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C: Accession: A70573
R: Cole, S.T.; Broscb, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Qy 1 GPHETI 8
Db 16 GEHETI 23

RESULT 17
T40860 probable alpha-amylase precursor SPCC11E10.09c - fission yeast (Schizosaccharomyces pombe)
C: Species: Schizosaccharomyces pombe
C: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C: Accession: T40860; T41181
R: Ramspacher, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, October 1999
A: Reference number: 221952
A: Accession: T40860
A: Status: translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-478 <RAM>
A: Cross-references: UNIPROT:Q10427; EMBL:AL121783; PIDN:96016988; PID:96016988; PID:96106988
A: Experimental source: strain 972h-; cosmid C11E10
R: Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
A: Reference number: 221976
A: Accession: T41181
A: Status: translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-203 <LYN>
A: Cross-references: EMBL:AL049662; PID:94578680; PIDN: CAB41221.1; PID:94678681; PID:94678681; GSPDB:GN
A: Experimental source: strain 972h-; cosmid C11E8
C: Genetics:
A: Gene: SPDB:SPCC11E10.09c; SPDB:SPCC11E10.09c
A: Map position: 3
A: Intron: 320/3; 468/3
C: Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
Query Match 70.8%; Score 34; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
Db 168 PHETIT 173

RESULT 18
G82971 probable ferredoxin PA5399 [imported] - Pseudomonas aeruginosa (strain PAO1)
C: Species: Pseudomonas aeruginosa
C: Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C: Accession: G82971
C: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, R.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: G82971
 A;Status: preliminary
 A;Cross-references: UNIPROT:09HTG5; GB:AE004952; PIDN:AAG0978
 A;Experimental source: strain PA01
 A;Genetics:
 A;Gene: PA5399

Query Match 70.8%; Score 34; DB 2; Length 653;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHEITITAL 9
 ||||: |||
 Db 301 GPHQPIVNL 309

RESULT 19
 D87196 probable membrane protein [imported] - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: D87196
 R;Cole, S.T.; Eigmairer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd, R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Fraser, A.; Hamlin, N.; Hamlin, N.; Rutherford, K.M.; Nature, M.A.; Rutherford, K.M.; Nature, M.A.; Authors: Rutter, S.; Seeger, K.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Title: Massive gene decay in the leprosy bacillus.
 A;Reference number: A86909; MUID:21128732; PMID:112334002
 A;Accession: D87196
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-181 <STO>
 A;Cross-references: UNIPROT:09CB97; GB:AL450380; PIDN:G13093921; GSPDB:G
 C;Genetics:
 C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2669

Query Match 68.8%; Score 33; DB 2; Length 181;
 Best Local Similarity 55.6%; Pred. No. 25;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPHEITITAL 9
 ||||: |||:
 Db 130 GPHQPIESV 138

RESULT 20
 C70510 hypothetical protein Rv2696c - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: C70530
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature, M.A.; Nature, M.A.; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: C70530
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-259 <COL>
 A;Cross-references: UNIPROT:007198; GB:Z96072; PIDN:G3261793; PIDN:CA09486
 C;Genetics:
 C;Gene: Rv2696c

A;Title: The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1
 A;Reference number: A30083 ; MUID:98274327 ; PMID:2839594
 A;Accession: H30084
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-355 <HEI>
 A;Cross-references: UNIPROT:PI0210 ; GB:X14112 ; NID:g1944536 ; PMID:CAA32318.1 ; PMID:g59526;
 C;Genetics:
 C;Superfamily: varicella-zoster virus gene 33 protein
 C;Keywords: capsid protein

RESULT 30
 D82452 anaerobic ribonucleoside-triphosphate reductase VCA0511 [imported] - *Vibrio cholerae* (st)
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82452
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamatshavan, J.; Basu, S.; Qin, H.; Dragoi, I.; Sellers, P.
 J., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Accession number: A82035 ; MUID:20406833 ; PMID:10952301
 A;Accession: D82452
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-706 <HEI>
 A;Cross-references: UNIPROT:Q9KM77 ; GB:AE004381 ; NID:AE003853 ; PMID:g9657902 ; PIDN:AAF96414
 C;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VCA0511
 A;Map position: 2
 C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase; c
 ide-triphosphate reductase middle homology; rubredoxin homology
 C;Keywords: iron; metalloprotein
 C;Binding site: iron (Cys) #status predicted
 Query Match 68.8% ; Score 33 ; DB 2 ; Length 706 ;
 Best Local Similarity 77.8% ; Pred. No. 1.2e-02 ;
 Matches 7 ; Conservative 0 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;
 Qy 1 GPHETITAL 9
 Db 473 GTNETTIAL 481

RESULT 31
 A64047 ribonucleoside-triphosphate reductase, oxygen-sensitive (EC 1.17.4.-) - *Haemophilus influenzae*
 C;Species: *Haemophilus influenzae*
 C;Accession: A64047
 C;Date: 18-Aug-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kerlavage, A.
 ;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman, J.
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
 A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A;Accession: A64047
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Residues: 1-707 <HEI>
 A;Molecule type: DNA
 A;Accession: A64047
 A;Status: nucleic acid sequence not shown; translation not shown

A;Cross-references: UNIPROT:P43752; GB:U32893; GB:L42023; NID:91573021; PID: AAC21751.1
 C;Comment: This enzyme must be activated by the anaerobic ribonucleotide reductase activ
 es peptide cleavage.
 C;Function:
 A;Description: catalyzes the reduction by reduced thioredoxin of a ribonucleoside triph
 o
 A;Pathway: deoxyribonucleotide biosynthesis
 A;Note: this enzyme is different both from ribonucleoside-triphosphate reductase (EC 1.1
 nds iron and has a tyrosyl radical
 C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
 ide-triphosphate reductase middle homology; rubredoxin homology
 C;Accession: A47331; SS6464;
 R;Sun, X.; Harder, J.; Krook, M.; Jornvall, H.; Sjoberg, B.M.; Reichard, P.
 Proc. Natl. Acad. Sci. U.S.A. 90, 577-581, 1993
 Article: A possible Glycine radical in anaerobic ribonucleotide reductase from Escherich
 i
 A;Reference number: A47331; MUID:9313381; PMID:8421692
 A;Accession: A47331
 A;Molecule type: DNA; Protein
 A;Residues: 1-256, 'R', 'P', '421-712 <SUN>
 A;Cross-references: UNIPROT:P28903; GB:L06097; NID:9146968; PID:AAA4226.1; PID:g146970
 A;Cross-references: EMBL:U14003; PID:g1263172; PID:9537080
 A;Note: sequence extracted from NCBI Backbone (NCBIN122819, NCBI:122819)
 A;Note: parts of this sequence, including the amino end of the mature protein, were de
 R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 23, 2105-2119, 1995
 Article: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
 A;Reference number: S56314; MUID:95334162; PMID:7610040
 A;Accession: S56314
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-712 <BUR>
 A;Cross-references: EMBL:U14003; PID:g1263172; PID:9537080
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 Article: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426517; PMID:9278503
 A;Accession: A65236
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-712 <BLAT>
 A;Cross-references: GB:AB00495; GB:U0096; NID:92367361; PID: AAC77195.1; PID:g1790686;
 A;Experimental source: strain K-12, substrate MG1655
 C;Comment: This enzyme must be activated by the anaerobic ribonucleotide reductase activ
 es peptide cleavage.
 C;Genetics:
 A;Gene: nrdD
 A;Complex: homodimer
 C;Function:
 A;Cross-references: UNIPROT:P43752; GB:U32893; GB:L42023; NID:91573021; PID: AAC21751.1
 A;Pathway: deoxyribonucleotide biosynthesis
 A;Description: catalyzes the reduction by reduced thioredoxin of a ribonucleoside triph

A;Note: this enzyme is different both from ribonucleoside-triphosphate reductase (EC 1.1.1.1) and has a tyrosyl radical and has a tyrosyl radical oxygen-sensitive ribonucleoside-triphosphate reductase; C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase; C;Keywords: deoxyribonucleotide biosynthesis; homodimer; iron; metalloprotein; oxidoreductase; C;Accession: FJ96-729/Domain: oxygen-sensitive ribonucleoside-triphosphate reductase middle homology * FJ305-706/Domain: oxygen-sensitive ribonucleoside-triphosphate reductase carboxyl-terminal FJ644-647/Domain: rubredoxin homology #status acypical <RUB> FJ644-647/662,665/Binding site: iron (Cys) #status predicted FJ681/Active site: Gly (stable glycyl radical) #status predicted	
Query Match 68.8%; Score 33; DB 1; Length 712; Best Local Similarity 77.8%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy 1 GPHTETIAL 9	
Db 493 GHETTINAL 501	
RESULT 33	
AC1058 ribonucleoside-triphosphate reductase (EC 1.17.4.2) - <i>Salmonella enterica</i> subsp. <i>enterica</i>	
C;Species: <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i>	
A;Note: this species has also been called <i>Salmonella typhi</i>	
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002	
C;Accession: AC1058	
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gara, P.	
Nature 413, 848-852, 2001	
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar	
A;Reference number: AB0502; MUID:21534947; PMID:11677608	
A;Accession: AC1058	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-712 <PAR>	
A;Cross-references: GB:AL513382; PIDN:CA006912.1; PID:gi16505560; GSPDB:GN001176	
C;Genetics:	
C;Gene: nrdd	
C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase; C;Keywords: iron; metalloprotein; oxidoreductase	
C;Accession: FJ644-647/662,665/Binding site: iron (Cys) #status predicted	
Query Match 68.8%; Score 33; DB 2; Length 712; Best Local Similarity 77.8%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy 1 GPHTETIAL 9	
Db 493 GHETTINAL 501	
RESULT 34	
G91280 anaerobic ribonucleoside-triphosphate reductase [imported] - <i>Escherichia coli</i> (strain O1	
C;Species: <i>Escherichia coli</i>	
C;Accession: G91280	
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004	
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Goto, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
DNA Res. 8, 11-22, 2001	
A;Title: Complete genome sequence of enterohemorrhagic <i>Escherichia coli</i> O157:H7 and geno	
A;Reference number: A99629; MUID:21156231; PMID:11258795	
A;Accession: G91280	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-712 <HAY>	
A;Cross-references: UNIPROT:Q8XCE2; GB:BA000007; PIDN:BAB38638.1; PID:gi13364692; GSPDB:G	
A;Experimental source: strain O157:H7; substrain RIMD 050952	
C;Genetics:	

A;Gene: EC55215
 C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
 C;Keywords: iron; metalloprotein
 F;644,647,662,665/Binding site: iron (Cys) #status predicted

Query Match Score 68.8%; Best Local Similarity 77.8%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETTIAL 9
 Db 493 GIHETINAL 501

RESULT 35

G86121 anaerobic ribonucleoside-triphosphate reductase [imported] - Escherichia coli (strain O1

C;Species: Escherichia coli
 C;Accession: G86121
 C;Cross-references: UNIPROT:G86121

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Ross, D.J.; Mayhew, Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G86121
 A;Status: preliminary

C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;

C;Keywords: iron; metalloprotein
 F;644,647,662,665/Binding site: iron (Cys) #status predicted

Query Match Score 68.8%; Best Local Similarity 77.8%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETTIAL 9
 Db 493 GIHETINAL 501

RESULT 36

AG0419 ribonucleoside-triphosphate reductase (EC 1.17.4.2) [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
 C;Accession: AG0419
 C;Cross-references: UNIPROT:AG0419

R;Pritchill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB00001; MUID:21470413; PMID:11586360

A;Accession: AG0419
 A;Molecule type: DNA
 A;Residues: 1-712 <KTR>

C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
 C;Keywords: iron; metalloprotein
 F;644,647,662,665/Binding site: iron (Cys) #status predicted

Query Match Score 68.8%; Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
 Db 920 PHETVT 925

RESULT 37
 T30542 major surface glycoprotein - Pneumocystis carinii (fragment)

C;Species: Pneumocystis carinii
 C;Accession: T30542
 C;Cross-references: EMBL:AF033212; PID:93560521; PIDN: AAC34975.1

A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari

A;Accession: AG0419
 A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
 A;Residues: 1-1008 <MEI>

C;Cross-references: EMBL:AF033212; PID:93560521; PIDN: AAC34975.1

C;Genetics: MSG
 C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match Score 68.8%; Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETTIAL 9
 Db 492 GIHETINAL 500

probable membrane protein YMR288w - Yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein YM0021.14
 C;Species: Saccharomyces cerevisiae
 C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S54595
 R;Pearson, D.; Bowman, S.
 submitted to the EMBL Data library, May 1995
 A;Reference number: S54582
 A;Accession: S54595
 A;Molecule type: DNA
 A;Residue: 1-971 <PEA>
 A;Cross-references: UNIPROT:P49955; EMBL:Z49704; PID:9825540; PID:982554; GSPDB:GN00013;
 A;Experimental source: strain AB972
 C;Genetics:
 A;Gene: SGD:HSH155; MIPS:YMR288w
 A;Cross-references: SGD:S0004901
 A;Map position: 13R
 C;Keyword: transmembrane protein
 F;333-349:Domain: transmembrane #status predicted <TM1>
 F;777-793:Domain: transmembrane #status predicted <TM2>

Query Match Score 68.8%; Best Local Similarity 55.6%; Pred. No. 1.6e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETTIAL 9
 Db 758 GPHDVLYAL 766

RESULT 38
 T30544 major surface glycoprotein - Pneumocystis carinii (fragment)

C;Species: Pneumocystis carinii
 C;Accession: T30544
 C;Cross-references: EMBL:AF033212; PID:93560521; PIDN: AAC34975.1
 R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.

A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari

A;Accession: AG0419
 A;Status: preliminary

C;Cross-references: EMBL:AF033212; PID:93560521; PMID:98380374; PMID:9712777

A;Molecule type: DNA
 A;Residues: 1-1008 <MEI>

C;Cross-references: EMBL:AF033212; PID:93560521; PIDN: AAC34975.1

C;Genetics: MSG
 C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match Score 68.8%; Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
 Db 920 PHETVT 925

RESULT 39
 T30542 major surface glycoprotein - Pneumocystis carinii (fragment)

C;Species: Pneumocystis carinii
 C;Accession: T30542
 C;Cross-references: EMBL:AF033212; PID:93560521; PIDN: AAC34975.1

A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari

A;Accession: AG0419
 A;Molecule type: DNA
 A;Residues: 1-712 <KTR>

C;Cross-references: EMBL:AF033212; PID:93560521; PIDN: AAC34975.1

C;Genetics: MSG
 C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

C;Accession: T30542
R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis carinii
A;Reference number: 217905; PMID:9830374; PMID:9712777
A;Accession: T30542
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1017 <MEI>
A;Cross-references: EMBL:AF033210; NID:93560516; PID:93560517; PIDN: AAC34973.1
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 68.8%; Score 33; DB 2; Length 1017;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
Db 912 PHETVT 917

RESULT 40

T30543
major surface glycoprotein - Pneumocystis carinii (fragment)
C;Species: Pneumocystis carinii
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C;Accession: T30543
R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis carinii
A;Reference number: 217905; PMID:9830374; PMID:9712777
A;Accession: T30543
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1022 <MEI>
A;Cross-references: EMBL:AF033211; NID:93560518; PID:93560519; PIDN: AAC34974.1
C;Genetics:
A;Gene: MSG
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 68.8%; Score 33; DB 2; Length 1022;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
Db 915 PHETVT 920

RESULT 41

C36792
hypothetical protein ORF56 - ictalurid herpesvirus 1 (strain auburn 1)
C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: C36792
R;Davidson, A.J.
R;Submitted to GenBank, January 1992
A;Description: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A36804
A;Accession: C36792
A;Molecule type: DNA
A;Residues: 1-1179 <DAV>
A;Cross-references: UNIPROT:Q00099; GB:M75136; NID:g331209; PID:g331266
R;Davidson, A.J.
R;Title: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A39447; MUID:92087490; PMID:1727613
A;Contents: annotation
A;Note: neither protein nor nucleic acid sequence is given
C;Genetics:

A;Gene: 56
C;Superfamily: ictalurid herpesvirus 1 hypothetical protein ORF56
Query Match 68.8%; Score 33; DB 2; Length 1179;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GPHEIT 7
Db 828 GPHGTIT 834

RESULT 42

MWXR31
lambda 3 protein - reovirus type 1 (strain Lang)
N;Alternate names: minor core protein
C;Species: reovirus type 1
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: A30121
A;Molecule type: Genomic RNA
A;Residues: 1-1267 <WIB>
A;Cross-references: UNIPROT:P17376; GB:M24734; NID:g499863
A;Note: this sequence, which matches the sequence attributed to type 1 in Fig. 2, matches the sequence in entries REO1LAM3P and REO3LAM3P now differ only by the sequence correction
C;Comment: See also PIR:MWXR33.
C;Genetics:
A;Map position: segment L1
C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein
Query Match 68.8%; Score 33; DB 1; Length 1267;
Best Local Similarity 71.4%; Pred. No. 2.e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PHETITA 8
Db 105 PHETLTS 111

RESULT 43

MWXR32
lambda 3 protein - reovirus type 2 (strain D5/Jones)
N;Alternate names: minor core protein
C;Species: reovirus type 2
C;Accession: B30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: B30121
A;Molecule type: Genomic RNA
A;Residues: 1-1267 <WIB>
A;Cross-references: UNIPROT:P17377; GB:M31057; NID:g499865; PIDN:AAA47245.1; PID:g499866
C;Genetics:
A;Map position: segment L1
C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein
Query Match 68.8%; Score 33; DB 1; Length 1267;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PHETITA 8
Db 105 PHETLTS 111

RESULT 44
 MWXR33 Lambda 3 protein - reovirus type 3 (strain Dearing)
 N; Alternate names: minor core protein
 C; Species: reovirus type 3
 C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 A; Accession: C30121
 R; Wiener, J.R.; Joklik, W.K.
 Virology 169, 194-203, 1989.
 A; Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
 A; Reference number: A94390; MUID:89163254; PMID:2922925
 A; Accession: C30121
 A; Molecule type: genomic RNA
 A; Residues: 1-1267 <MIE>
 A; Cross-references: UNIPROT:P17378; GB: M31058; NID:9499867; GB: M24734; NID:9499863; PIDN
 A; Note: this sequence, which matches the sequence attributed to type 3 in Fig. 2, matches
 entries REO1LAM3P and REO3LAM3P now differ only by the sequence correction apparently made
 C; Comment: See also PIR:MWXR31.
 C; Genetics:
 A; Map position: segment L1
 C; Superfamily: reovirus lambda 3 protein
 C; Keywords: core protein

Query Match 68.8%; Score 33; DB 1; Length 1267;
 Best Local Similarity 71.4%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETITA 8
 Db 105 PHETLTS 111

RESULT 45
 T38353 serine hydroxymethyltransferase - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C; Accession: T38353
 R; Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 A; Reference number: Z211787
 A; Accession: T38353
 A; Molecule type: DNA
 A; Residues: 1-467 <MUR>
 A; Cross-references: UNIPROT:O13972; EMBL: Z98601; PIDN: CAB11269.1; GSPPDB:GN00066; SPDB:SF
 A; Experimental source: strain 972h; cosmid C24C9
 C; Genetics:
 A; Gene: SPDB:SPAC24C9.12c
 A; Map position: 1
 C; Superfamily: serine/glycine hydroxymethyltransferase

Query Match 67.7%; Score 32.5; DB 2; Length 467;
 Best Local Similarity 80.0%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GPH-ETITAL 9
 Db 288 GPHNHTITAL 297

RESULT 46
 T37918 serine hydroxymethyltransferase - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 R; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
 A; Reference number: Z211754
 A; Accession: T37918
 A; Status: preliminary; translated from GB/EMBL/DBJ

Qy 1 GPHETITAL 9
 ||| : |:

A; Molecule type: DNA
 A; Residues: 1-172 <CON>
 A; Cross-references: UNIPROT:Q10104; EMBL: Z68198; PIDN: CAA2384.1; GSPPDB:GN00066; SPDB:SP
 A; Experimental source: strain 972h; cosmid c18G6
 C; Genetics:
 A; Gene: SPDB:SPAC18G6.04C
 A; Map position: 1
 C; Superfamily: serine/glycine hydroxymethyltransferase

Query Match 67.7%; Score 32.5; DB 2; Length 472;
 Best Local Similarity 80.0%; Pred. No. 94;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GPH-ETITAL 9
 Db 294 GPHNHTITAL 303

RESULT 47
 A42241 glycine hydroxymethyltransferase (EC 2.1.1.2.1), cytosolic - Neurospora crassa
 N; Alternate names: serine hydroxymethyltransferase
 C; Species: Neurospora crassa
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C; Accession: A42241
 R; McClung, C.R.; Davis, C.R.; Page, K.M.; Denome, S.A.
 A; Title: Characterization of the formate (for) locus, which encodes the cytosolic serine
 A; Reference number: A42241; MUID:32195225; PMID:1532227
 A; Accession: A42241
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-479 <MC2C>
 A; Cross-references: UNIPROT:P24898; GB: M81918
 C; Superfamily: serine/glycine hydroxymethyltransferase
 C; Keywords: cytosol, phosphoprotein, pyridoxal phosphate; transferase (covalent) #status predicted
 F; Binding site: pyridoxal phosphate (Lys)

Query Match 67.7%; Score 32.5; DB 1; Length 479;
 Best Local Similarity 80.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GPH-ETITAL 9
 Db 294 GPHNHTITAL 303

RESULT 48
 T03782 probable lipid transfer protein - rice
 C; Species: Oryza sativa (rice)
 C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C; Accession: T03782
 R; Vignols, F.; Lund, G.; Phami, S.; Tremousaygue, D.; Kader, J.; Budiman
 Gene 142, 265-270, 1994
 A; Title: Characterization of a rice gene coding for a lipid transfer protein.
 A; Reference number: Z15081; MUID:9425278; PMID:194762
 A; Accession: T03782
 A; Molecule type: DNA
 A; Residues: -117 <VIG>
 A; Cross-references: UNIPROT:O42999; EMBL: Z23271; NID: 9510336; PIDN: CAA80809.1; PID: 95103:
 A; Experimental source: cv. IR36
 C; Genetics:
 A; Introns: 115/3
 C; Superfamily: phospholipid transfer protein

Query Match 66.7%; Score 32; DB 2; Length 117;
 Best Local Similarity 55.6%; Pred. No. 25;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
 ||| : |:

Db 20 GPHTTMAAI 28

RESULT 49

T0042 Lipid transfer protein LPT II - rice

C;Species: Oryza sativa (rice)

C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C;Accession: T0042

R.Iee, M.C.; Kim, C.S.; Eun, M.Y.

Submitted to the EMBL Data Library, August 1997

A;Description: Isolation and characterization of lipid transfer protein from rice.

A;Reference number: Z14508

A;Accession: T0042

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-118 <LTP2>

A;Cross-references: UNIPROT:O22483; EMBL:AF017359; PIDN:92407272; PIDN:AAH70539.1; PID:92

A;Experimental source: strain Millyang 23

C;Superfamily: phospholipid transfer protein

Qy 1 GPHTTITAL 9

Db 20 GPHTTMAAI 28

RESULT 50

T03300 probable lipid transfer protein precursor - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Accession: T03300

R.Ili, G.

Submitted to the EMBL Data Library, July 1995

A;Reference number: Z14895

A;Accession: T03300

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-118 <LIA>

A;Cross-references: UNIPROT:Q42978

A;Experimental source: strain Guang-lu-ai 4, shoot

C;Genetics:

A;Gene: LTP2

C;Superfamily: phospholipid transfer protein

F;26/Domain: Signal sequence #status predicted <SIG>

F;27-118/Product: lipid transfer protein #status predicted <MAT>

Qy 1 GPHTTITAL 9

Db 20 GPHTTMAAI 28

Search completed: July 27, 2005, 12:42:07

Job time : 56 secs

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Copyright (c) 1993 - 2005 CompuGen Ltd.	GenCore version 5.1.6	30	184.5	14.9	1259	2	T16038
OM protein - protein search, using sw model		31	183	14.8	191	2	F84522
Run on:	July 27, 2005, 12:03:22 ; Search time 40 Seconds (without alignments)	32	183	14.8	222	2	H96711
Title:	US-10-623-429-9_COPY_404_627	33	183	14.8	1460	1	EDBE1P
Perfect score:	1237	34	182.5	14.8	214	2	T10737
Sequence:	1 AIAADROAGGLPAAAGDHGI.....ALVNASSAAHVNDTARAAD 224	35	182.5	14.8	667	2	T17221
Scoring table:	BLOSUM62	36	182.5	14.8	1048	2	T31425
Gapopen:	10.0 , Gapext 0.5	37	180.5	14.6	280	2	T11671
Searched:	283416 seqs, 96216763 residues	38	180	14.6	322	2	S25299
Total number of hits satisfying chosen parameters:	283416	39	180	14.6	393	2	PQ0479
Minimum DB seq length: 0	40	180	14.6	439	2	S51939	
Maximum DB seq length: 2000000000	41	180	14.6	1201	2	G86441	
Post-processing: Minimum Match 10%	42	179.5	14.5	163	2	A29356	
Maximum Match 100%	43	179.5	14.5	309	2	S08343	
Listing First 45 summaries	44	179.5	14.5	369	2	S20500	
Database :	PIR 79:*	45	179.5	14.5	440	2	JC7807
	1: PIR1:*						
	2: pir2:*						
	3: pir3:*						
	4: pir4:*						
• Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	670.5	54.2	635	1 WMBW6	capсид protein - h		
2	221.5	17.9	522	2 S57216	viral proteinase - extensin-like homolog F		
3	215	17.4	699	2 T03225	68.6K capсид protein		
4	211	17.1	646	1 W2BBC8	hypothetical protein		
5	206	16.7	727	2 CB4534	hydroxyproline-rich extensin - Volvox		
6	204	16.5	620	2 A06733	extensin homolog T		
7	200	16.2	464	2 S22697	hypothetical protein		
8	198	16.0	760	2 T06291	phrophorin-S - V0		
9	196	15.8	929	2 C96623	proline-rich protein		
10	195.5	15.8	599	2 T10798	sulfated surface glycoprotein		
11	195	15.8	134	2 JC5572	hypothetical protein		
12	194.5	15.7	485	2 A33647	extensin CYC17 pre		
13	193	15.6	847	2 F96531	HPBII-7 protein -		
14	191.5	15.5	217	2 T09865	capidosome-associated protein		
15	190.5	15.4	551	2 S57447	extensin-like prot		
16	190.5	15.4	647	2 T42379	probable coil wall		
17	190	15.4	464	2 A47655	extensin-like protein		
18	189	15.4	1168	2 S49915	extensin homolog F		
19	188.5	15.2	428	2 E71415	hydroxyproline-rich		
20	187.5	15.2	839	2 T04859	hypothetical protein		
21	187	15.1	368	2 C29356	hypothetical protein		
22	187	15.1	907	2 B96336	hypothetical protein		
23	186.5	15.1	997	2 T28872	extensin-like protein		
24	186	15.0	1006	2 G86292	hypothetical protein		
25	185	15.0	242	2 S54156	extensin-like protein		
26	185	15.0	416	2 T34279	hypothetical protein		
27	185	15.0	760	2 F86387	probable protein kinase		
28	184.5	14.9	132	2 S14370	extensin class I (hypothetical protein)		
29	184.5	14.9	1018	2 T43168			
RESULT 2							
viral proteinase - rabies virus							
C;Species:	rabies virus						
C;Date:	07-May-1995	#sequence_revision	21-Jul-1995	#text_change	21-Aug-1998		
C;Accession:	S52216						
R;Camacho, A.; Tabaro, E.							
submitted to the EMBL Data Library, June 1994							
A;Reference number:	S52215						
A;Accession:	S52216						
A;Status:	Preliminary						
RESULT 1							
WMBW6	capid protein - human herpesvirus 1 (strain 17)						
C;Species:	human herpesvirus 1						
C;Date:	31-Dec-1989	#text_change	09-Jul-2004	#sequence_revision	31-Dec-1989		
C;Accession:	H30084						
R;McGeoch, D.J.; Dairymple, M.A.; Davison, A.J.; McNab, D.; Peri							
J. Gen. Virol. 69, 1531-1574, 1988							
A;Title:	The complete DNA sequence of the long unique region in the genome of herpes sim						
A;Reference number:	A30083; PMID:88274327						
A;Accession:	H30084						
A;Molecule type: DNA							
A;Residues: 1-35 (*MCG>							
A;Cross-references: UNIPROT:P10210; GB:X14112; NID:g1944536; PID:CAA32318.1; PID:g59526							
C;Genetics:							
C;Superfamily: varicella-zoster virus gene 33 protein							
C;Keywords: capsid protein							
Query Match	54.2%	Score 670.5;	DB 1;	Length 635;			
Best Local Similarity	63.4%	Pred. No. 2.5e-33;					
Matches	144;	Conservative	12;	Mismatches	64;	Indels	7;
Qy	1 AIAADQAGGLPAAAGDHGIGSARKERRHEQEPTDGDGRDPDQFGEADPDPBP 60						
Db	403 AIAADQAGGP-AAGDPGVRGSKERRYEGPSYCDQDBADPYYGEARQAPRG 461						
Qy	61 VDSRARQAOASGPHEITITALYGAITSQELAHMARRTHAPYGPYPVGPPVHADTE- 119						
Db	462 VDSRARHHSPTNTETALGAITSQELAHMARRTSAYGMITPAHVRPQVGEPEP 521						
Qy	120 TPAQQPPRYPKAVYLPPPHIAPPGPPPLSGA - VPPPSYPPVATPPGPAPPPLHOPSPAHAH 177						
Db	522 TTHPAICPPAVRPPHSAFPYGPQGPASHATPPYAPACPQPBP -- PCPSQT 578						
Qy	178 PBPPIPPEPTPPAASLQQPEAAGVAAEGALVNSAAHNVNDTARAAD 224						
Db	579 RAPLPTPAPFPAPANTGSQPEASNAEGALVNSAAHNVDVDTARAAD 625						

A; Molecule type: genomic RNA
 A; Cross-References: EMBL:X79983
 A; Note: the source is designated as pseudorabies virus
 C; Superfamily: varicella-zoster virus gene 33 protein

Query Match Score 221.5; DB 2; Length 522;
 Best Local Similarity 32.5%; Pred. No. 1.5e-06;
 Matches 89; Conservative 22; Mismatches 78; Indels 85; Gaps 19;
 • 1 AIAADRGAGGLPAAAGDHGIRGS-----AKRRRHEVEQPEYDCGRDEPDRDFFYPPG 52
 Qy 2744 APSLSSQLGAVSAMDRIHRRSPSPERPPARKRY-----DDYAQDNAYYQG 322
 Qy 53 EARPEPRTVDSRRAARQASGPHEITIALGAVTSIQLQELAHMRA---RTHAP-YGYPF- 107
 Db 323 EAPP-----PRATSRAV--VSSHQRETSHLRAQHVRVTPYVAPAPQ 363
 Qy 108 -----VG_PYHMPHADTTPAQSPRY_PAKAYVLLPP-----HMAP--PGPPUSGAPE 152
 Db 364 LLPPGAVVQGPQPHPH-HAAGA\NPPMYQPPGQHAPPSPVHAPVAPGLASBRCP 422
 Qy 153 -----PSYP-----PVAVTGPAPPL-----HQP_SPAHAHPP_PPPPGPTPPA 190
 Db 423 VAHHPAQVWVQQPVWVQAVQAVVAVPAAPPLQORHAAAPVQAAPAPASAQQPVQ 482
 Qy 191 ASL_PQEAAGAEGALVNASSAAAHYNDARAAD 224
 • Db 483 ASVSPAP-PTESPPAPIDASSAA---VACORGAD 512

RESULT 3
 T05225 extensin homolog F1715_160 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: T05225
 R;Bevan, M.; Vitale, D.; Lignori, R.; Argirou, A.; De Simone, V.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, July 1998
 A;Accession: T05225
 A;Molecule type: DNA
 A;Residues: 1-699 <BEV>
 A;Experimental source: cultivar Columbia; EAC clone F1715
 C;Genetics:
 A;Map position: 4
 A;Note: F1715_160

Query Match Score 215; DB 2; Length 699;
 Best Local Similarity 32.5%; Pred. No. 4.e-06;
 Matches 53; Conservative 17; Mismatches 65; Indels 28; Gaps 6;
 Qy 55 RPEP---RVDSSRAARQASGPHEITIALGAVTSIQLQELAHMRAHAP-----Y 103
 Db 482 KPSVPSRVRVQKQDPPKESPQDPDYD-----QSPVTKRSRPPPAVNSPPPPVY 532
 Qy 104 PYPPVGPYHMPHADTTPAQSPRY---PAKAYVLLPPHIAPGPPLSGAVPPSY---P 156
 Db 533 RPPVPPVHSPSPPPVYHSPSPPPVYHSPSPPPVYHSPSPPPVYHSPSPPPVYHSPSPPPVY 591
 Qy 157 PVAVTGPAPPLHOPSPAHAHPPPPGTTPPAASLDQPEAP 199
 Db 532 PVNSPPPPAPVHSPSPPPVYHSPSPPPVYHSPSPPPVYHSPSPSQSP 634

RESULT 4
 WZBEC8 67.6K capsid protein - equine herpesvirus 1 (strain Ab4D)
 C;Species: equine herpesvirus 1
 A;Note: Equus caballus (domestic horse)
 C;Accession: I36798

R;Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
 submitted to GenBank, March 1992
 A;Description: The DNA sequence of equine herpesvirus-1.
 A;Reference number: A36805
 A;Accession: I36798
 A;Molecule type: DNA
 A;Residues: 1-646 <TEL>
 A;Cross-references: UNIPROT:P28936; GB:MB86664; NID:9330791; PIDN:AA02470.1; PID:9330827
 R;Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
 Virology 189, 304-316, 1992
 A;Title: The DNA sequence of equine herpesvirus-1.
 A;Reference number: A41831; MUID:9229566; PMID:1318606
 A;Contents: annotation of possible protein-coding frames
 A;Note: neither amino acid nor nucleotide sequence is given
 C;Genetics:
 A;Gene: 35
 C;Superfamily: varicella-zoster virus gene 33 protein
 C;Keywords: capsid protein

Query Match Score 211; DB 1; Length 646;
 Best Local Similarity 30.9%; Pred. No. 7.e-06;
 Matches 77; Conservative 25; Mismatches 55; Indels 92; Gaps 12;
 Qy 1 AIAADRGAGGLPAAAGDHGIRGS-----AKRRRHEVEQPEYDCGRDEPDRD 46
 Db 413 ALAADRKA--TKGSDPHIVQGSCSPPPLSPQQERRVARKRRIIDWATRDRD----DLE 463
 Qy 47 FPYYPGEARPEPRFDSSRAARQASGPHEITIALGAVTSIQLQELAHMRA-----RTH 99
 Db 464 GIYYPGERSSPR--GERRAGR--PSTTIAIDLQAVGSSLQEVSQLRAIQTVTAQQA 516
 Qy 100 APYGPYPVGPYHMPHADTTPAQSPRYPAKAYVLLPPH-----IAPPGPPLSGAVPPPS 154
 Db 517 APAGLYKP-----PAVPPQI-SQYQYIOPHAWSAIVAPOLPGI-----PS 557
 Qy 155 YPPVAVTGPAPPLHQSPSPAHAHPPPPGPTPPAASLPQPPAPGAEAGALVNASSAH 214
 Db 558 QPQVQAVL-----APQVPAEGAPS---AKVVAASTAP 586
 Qy 215 VNVDTARAA 223
 Db 587 QQAEQARAA 595

RESULT 5
 C8534 hypothetical protein At2g15880 [Imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: C84334
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: C84334
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-727 <STO>
 A;Cross-references: UNIPROT:Q9XIL9; GB:AE002093; NID:95306245; PIDN:AA041978.1; GSPDB:GN
 A;Genes: At2g15880
 A;Map position: 2

Query Match Score 206; DB 2; Length 727;
 Best Local Similarity 29.0%; Pred. No. 1.7e-05;
 Matches 72; Conservative 16; Mismatches 86; Indels 74; Gaps 14;
 Qy 2 IAADRGAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDE-----PD 44
 Db 349 IALDDTRNCLP---DRPKQRSACEAVVSRP-VDCSDKRCAGGSSQATPSKSPPSPVPT 403

Best Local Similarity 27.1%; Pred. No. 8.2e-05; Matches 67; Conservative 22; Mismatches 96; Indels 62; Gaps 10; Qy 13 AAAGDGHGIRSAKRRHEVQPE-----YFG 52 Db 202 SAGSDYGGGGKQSQSKPAPGGGSFSSPSQTHGGGRSPPLPQFTAGNASFFS 261 Qy 53 EARPEPRVDSRRAARQASGPHEITALYG-----AVTSI-----QELAMMRARTHAPGP 104 Db 262 STQPPGQTMAGNAPSSTPPLPGOYPAVNAQLSTSAPSVP 321 Qy 105 YPPGPYHHPADETPAQPPRPAKAVVLP-----PPIAARG 143 Db 322 LPP-CQYTAVNAPPSTSTQVSLP-PGOMPGNAALSASTPLPQGFTANAPD--APG 377 Qy 144 PPLSAVPPSYPVAVTPAPPLHQPSPAHAHPPPPG-----PPPPPASLQPE 197 Db 378 PANQTSPPPPPSAAPPSSPKKGPKA--APPPPPGKKGAGPPPPNPKKGPK 434 Qy 198 APGAEG 204 Db 435 PPGNPKG 441

RESULT 10

T10798

pherophorin-S - Volvox carteri

C;Species: Volvox carteri

C;Accession: T10798

R;Godl, K.; Hallmann, A.; Wanzl, S.; Sumpf, M.

EBO J. 16, 25-34, 1997

A;Title: Differential targeting of closely related ECM-glycoproteins: The pherophorin f

A;Reference number: Z1154; MUID:97162277; PMID:909264

A;Status: preliminary;

A;Molecule type: mRNA

A;Cross-references: UNIPROT:PI21997; GB:X51616; NID:921999; PIDN:CAA35953.1; PID:gi1405821

Query Match 15.8%; Score 19.5%; DB 2; Length 99; Best Local Similarity 42.6%; Pred. No. 6e-05; Matches 43; Conservative 3; Mismatches 40; Indels 15; Gaps 3; C;Keywords: extracellular matrix; glycoprotein; pheromone

Query Match 15.8%; Score 19.5%; DB 2; Length 99; Best Local Similarity 42.6%; Pred. No. 6e-05; Matches 43; Conservative 3; Mismatches 40; Indels 15; Gaps 3; C;Keywords: extracellular matrix; glycoprotein; pheromone

Qy 99 HAPYGPYPVGPYHHPADETTPAOPPRYPAKAVYLPPPHIAAPGPPPLSAGVPPPSYPPV 158 Db 216 NAPPSPLPSSPPP-----PSPPPSPP-----PSPPPSPPSPPSPPSPPSPP 263

Qy 159 AVTGPAPLHQPSPAHAHPPPPGPPGPPPAASLQPEAP 199 Db 264 PPPPPPSSPPP-----PSPPPSPP-----PSPPPSPPSPPSPPSPP 301

RESULT 11

JC5572

proline-rich protein P-B1 precursor - human

C;Species: Homo sapiens (man)

C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004

C;Accession: JC5572

R;Isemura, S.; Saitoh, E.

J. Biochem. 121, 1025-1030, 1997

A;Title: Nucleotide sequence of gene B1 encoding a protein homologous to salivary proline-rich protein P-B1.

A;Reference number: JC5572; MUID:98014462; PMID:9354371

A;Accession: JC5572

A;Molecule type: DNA

A;Residues: 1-134 <ISEE>

A;Cross-references: UNIPROT:Q99934; DDBJ:089501; NID:91854451; PIDN:BA113971.1; PID:9185

C;Comment: This protein plays roles in the maintenance of teeth by inhibiting crystal formation from the digestive organs.

C;Genetics:

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Result No.	Score	Query	Match	Length	DB	ID	Description
1	670.5	Sequence 2, Appli	635	4	US-08-176-320-2		Sequence 2, Appli
2	660.0	Sequence 2, Appli	635	1	US-07-032-855-2		Sequence 2, Appli
3	190.5	Sequence 7961, Ap	553	4	US-09-949-016-7961		Sequence 7961, Ap
4	189.5	Sequence 7664, Ap	324	4	US-09-949-016-7664		Sequence 7664, Ap
5	189.5	Sequence 7108, Ap	498	4	US-09-949-016-7108		Sequence 7108, Ap
6	184.5	Sequence 2, Appli	559	4	US-10-116-370-2		Sequence 2, Appli
7	184.5	Sequence 10952, A	567	4	US-09-949-016-10952		Sequence 10952, A
8	184	Sequence 6, Appli	297	2	US-08-080-555B-6		Sequence 6, Appli
9	184	Sequence 6, Appli	297	3	US-09-262-653A-6		Sequence 6, Appli
10	179	Sequence 2904, Ap	511	4	US-09-433-2904		Sequence 2904, Ap
11	178.5	Sequence 24873, A	142	4	US-09-252-991A-2873		Sequence 24873, A
12	178	Sequence 235, App	104	4	US-09-547-693-235		Sequence 235, App
13	178	Sequence 278, App	707	4	US-09-919-039-278		Sequence 278, App
14	178	Sequence 993, App	707	4	US-09-338-092-993		Sequence 993, App
15	178	Sequence 10120, A	735	4	US-09-949-016-10120		Sequence 10120, A
16	177.5	Sequence 998, Ap	581	4	US-09-949-016-9978		Sequence 998, Ap
17	177	Sequence 4, Appli	214	1	US-08-217-327-4		Sequence 4, Appli
18	177	Sequence 21050, A	143	4	US-09-248-798A-21050		Sequence 21050, A
19	177	Sequence 19531, A	971	4	US-09-248-798A-19531		Sequence 19531, A
20	176.5	Sequence 2, Appli	1274	3	US-09-059-443-2		Sequence 2, Appli
21	175.5	Sequence 11282, A	506	4	US-09-949-016-11282		Sequence 11282, A
22	175.5	Sequence 9, Appli	684	4	US-09-83-244A-9		Sequence 9, Appli
23	175	Sequence 42632, A	288	4	US-09-209-767-42632		Sequence 42632, A
24	175	Sequence 2, Appli	503	4	US-09-599-287A-2		Sequence 2, Appli
25	175	Sequence 24, Appli	507	4	US-09-599-287A-24		Sequence 24, Appli
26	173.5	Sequence 2, Appli	1248	2	US-09-000-897-2		Sequence 2, Appli
27	173.5	Sequence 19, Appli	1248	3	US-09-323-735-2		Sequence 19, Appli

Db 462 VDSRRAARASPGTNETITALMGAUTSLOELAHRARTSAPGMYTPVHYRQVGEPEP 521 RESULT 3
 Qy 120 TPAQPPRYAKAVLPPPHIAAPPPLSSGA- VPPPSYPVAVTPGPAPDPLHOPSPAH 177 ; Sequence 7961, Application US/0949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 7961
 ; LENGTH: 553
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7961

Db 522 TTHPALCPEAVRPPAASLQPEAPGAEAGALVNASSAAHVNDTARAAD 578

Db 579 RAPLTERAPPARTGSQPEASNAEAGALVNASSAAHVNDTARAAD 625

RESULT 2
 Sequence 2, Application US/07812855
 Patent No. 547827
 GENERAL INFORMATION:
 APPLICANT: Roizman, Bernard
 APPLICANT: Liu, Penyong
 TITLE OF INVENTION: Methods and Compositions of a
 TITLE OF INVENTION: Preparation and use of A Herpes Protease
 NUMBER OF SEQUENCES: 15
 NUMBER OF SEQUENCES: 15
 ADDRESSSEE: ARNOLD, WHITE & DURKEE
 STREET: 321 No. 54 78727th Clark Street, Suite 800
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/832,855
 FILING DATE: 19920207
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coolley, Ronald B.
 REFERENCE DOCKET NUMBER: ARCD045
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 245-0090
 TELEFAX: (312) 245-0961
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 635 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-832-855-2

Query Match Best Local Similarity 53.4%; Score 660.5; DB 1; Length 635;
 Matches 142; Conservative 12; Mismatches 65; Indels 7; Gaps 4;
 Qy 1 AIAADROAGGLPAAGDGRIGSAKRRRHEVQEPEYDGRDDEDRDPPYYPEARPEPR 60
 ; Sequence 7664, Application US/0949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 7664
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7664

Db 403 AIAADROAGCQP-AAGDPVRSCKRREYEAQPSSESYCDDEDPYYPEARGAQPR 461

Db 61 VDSRRAARASGPHETITALVGAVTSLOELAHRARTSAPGMYTPVHYRQVGEPEP 119

Db 462 VDSRRAARASPGTNETITALMGAUTSLOELAHRARTSAPGMYTPVHYRQVGEPEP 521

Db 522 TTHPALCPEAVRPPAASLQPEAPGAEAGALVNASSAAHVNDTARAAD 578

Query Match Best Local Similarity 53.4%; Score 660.5; DB 1; Length 635;
 Matches 142; Conservative 12; Mismatches 65; Indels 7; Gaps 4;
 Qy 120 TPAQPPRYAKAVLPPPHIAAPPPLSSGA- VPPPSYPVAVTPGPAPDPLHOPSPAH 177
 ; Sequence 7931, Application US/0949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 7931
 ; LENGTH: 553
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7931

Db 579 RAPLTERAPPARTGSQPEASNAEAGALVNASSAAHVNDTARAAD 625

Query Match Best Local Similarity 39.3%; Score 190; DB 4; Length 324;
 Matches 48; Conservative 8; Mismatches 42; Indels 24; Gaps 7;
 Qy 178 PPPPPGPTPPAASLQPEAPGAEAGALVNASSAAHVNDTARAAD 224
 ; Sequence 7931, Application US/0949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 7931
 ; LENGTH: 553
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7931

Qy 100 APYGP----YPPVGVYHHPADTEPAQPPRPPAKAVLPPPHIAPPG---PPLSERV 150

RESULT 5

US-09-949-016-7108

Patent No. 6812319

SEQUENCE 7108, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 7108

LENGTH: 498

TYPE: PRT

ORGANISM: Human

US-09-949-016-7108

Query Match 14.9%; Score 184.5; DB 4; Length 559;

Best Local Similarity 31.5%; Pred. No. 1.2e-06; Mismatches 13; Indels 45; Gaps 9;

Matches 63; Conservative 63; Mi matches 79; Indels 45; Gaps 9;

55 RP-BPPVDSRRAARQASGPHEITALVGAVTSLQQELAHMRARTHAPYGPYPPVGPYHH 113

274 RPHEPPPPMHGACDAKIPCTCSATGLIENRQSPA--TGRPVEFVSPTPPPPPPL 331

Qy 114 PHADDBTAQPPRYPAKAVYLPPPHIAAPPVPPSYP--LSCGAVPPPSYP---LSCGAVPPPSYP---PVAVTPGP 164

Db 332 PSALSTSSLR---ASMTSTPPVPPPPPATLQAPAVPPPPQIAPGVLHHPAP 200

Qy 165 ---APPLHOPSPAHH-----PPBPPPGTTPPPASLPPPEAPG 200

Db 387 PPIAPPVQSPPPVRAAPVCPETVPHLPQGEVQGLPPPPPPPLPPPGI--RSPSP- 442

Qy 201 AEAGGLVNAASSAAHTNVDTA 220

Db 443 VTVTALAHPPSGLHLPTPSTA 462

RESULT 7

US-09-949-016-10952

Sequence 10952, Application US/09949016

Patent No. 6812319

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 7102

LENGTH: 567

TYPE: PRT

ORGANISM: Human

US-09-949-016-10952

Query Match 14.9%; Score 184.5; DB 4; Length 567;

Best Local Similarity 31.5%; Pred. No. 1.2e-06; Mismatches 13; Indels 45; Gaps 9;

Matches 63; Conservative 63; Mi matches 79; Indels 45; Gaps 9;

55 RP-BPPVDSRRAARQASGPHEITALVGAVTSLQQELAHMRARTHAPYGPYPPVGPYHH 113

282 RPHEPPPPMHGACDAKIPCTCSATGLIENRQSPA--TGRPVEFVSPTPPPPPPL 339

Qy 114 PHADDBTAQPPRYPAKAVYLPPPHIAAPPVPPSYP--LSCGAVPPPSYP---LSCGAVPPPSYP---PVAVTPGP 164

Db 340 PSALSTSSLR---ASMTSTPPVPPPPPATLQAPAVPPPPQIAPGVLHHPAP 394

Qy 165 ---APPLHOPSPAHH-----PPBPPPGTTPPPASLPPPEAPG 200

Db 395 PPIAPPVQSPPPVRAAPVCPETVPHLPQGEVQGLPPPPPPPLPPPGI--RSPSP- 450

Qy 201 AEAGGLVNAASSAAHTNVDTA 220

Db 451 VTVTALAHPPSGLHLPTPSTA 470

RESULT 8

US-08-580-545B-6

Sequence 6, Application US/08580545B

Patent No. 5332713

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: PABLO, A POLYPEPTIDE THAT INTERACTS WITH BCL-XL, AND

TITLE OF INVENTION: PABLO, A POLYPEPTIDE THAT INTERACTS WITH BCL-XL, AND

FILE REFERENCE: AM100012-D2

CURRENT APPLICATION NUMBER: US/10/116,370

CURRENT FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 2

LENGTH: 559

TYPE: PRT

ORGANISM: Homo sapiens

US-10-116-370-2

APPLICANT: Koichi, Fujisawa
 APPLICANT: Susumu, Nishiguchi
 APPLICANT: Yoshihiko, Maekawa
 APPLICANT: Randy, Allen
 ATTORNEY: Fish & Richardson P.C.
 TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 STREET: 601 Thirteenth Street, NW
 CITY: Washington
 STATE: DC
 COUNTY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08-580,545B
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Bretschneider, Barry E.
 REGISTRATION NUMBER: 28,055
 REFERENCE/DOCKET NUMBER: 04473/068001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/783-5070
 TELEFAX: 202/783-2331
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 297 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-580,545B-6

Query Match 14.9%; Score 184; DB 2; Length 297;
 Best Local Similarity 40.8%; Pred. No. 6.7e-07;
 Matches 42; Conservative 4; Mismatches 51; Indels 6; Gaps 3;

Qy 98 THA**P**G**P**V**G**P**H**P**H**A**D**T**P**A**Q**P**R**P**A**K**V**L**P**P**H**I**A**P**G**P**-**P**L**S**G**A**V**P**P**S**P** 156
 Db 105 T**K**A**T**P**P**K**P**K**P**-A**P**T**K**A**T**P**P**K**P**A**P**T**K**A**T**P**P**K**P** 162

Qy 157 P**V**A**T**P**G**P**A**P**L**H**O**P**S**P**A**H**A**H**P**P**P**P**P**P**P**A**S**L**P**O**E**P**A**P 199
 Db 163 P---T**P**A**P**P**V**K**A**T**P**P**T**P**K**A**T**P**T**P**K**A**T**P**V**K**A**T**P**T**P**P 202

RESULT 10
 US-09-107-433-2904
 Sequence 2904, Application US/09107433
 Patent No. 6800744
 GENERAL INFORMATION:
 APPLICANT: Lynn A. Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS
 NUMBER OF SEQUENCES: 5206
 CURRENT APPLICATION DATA:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinieillo, Pamela Daneke
 APPLICATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)93-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 2904:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 511 amino acids


```

; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: Curapart SeqFormatter Version 0.9
; SEQ ID NO: 993
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P23246
; US-09-538-092-993

Query Match 14.4%; Score 178; DB 4; Length 707;
Best Local Similarity 39.7%; Pred. No. 4; 8e-06;
Matches 46; Conservative 6; Mismatches 40; Indels 24; Gaps 6;
Qy 103 GPYPPVGPYHPPADTETPAQPPRYAKAVYLPPPHIAPPGP-PLSGAVVPPP----SYP 156
Db 55 GPKPKTPP-PPPHQQQQP--PQQQPPP--PQQQPPPQQPHQPHQPHQPHQPHQPOQSSKP 109

Query Match 14.4%; Score 178; DB 4; Length 707;
Best Local Similarity 39.7%; Pred. No. 4; 8e-06;
Matches 46; Conservative 6; Mismatches 40; Indels 24; Gaps 6;
Qy 157 PVAATPPAPPLHQPSPAAHAPP-----PPPGTTPPPASLPPPEAP 199
Db 110 VVAQGPSPAPGVSAPPASSAPPATPPTSGAAPPGGSPGPPTPTPPAVTSAPPAP 165

RESULT 15
US-09-949-016-10120
; Sequence 10120, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10120
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10120

Query Match 14.4%; Score 178; DB 4; Length 735;
Best Local Similarity 39.7%; Pred. No. 5e-06;
Matches 46; Conservative 6; Mismatches 40; Indels 24; Gaps 6;
Qy 103 GPYPPVGPYHPPADTETPAQPPRYAKAVYLPPPHIAPPGP-PLSGAVVPPP----SYP 156
Db 83 GPKPKTPP-PPPHQQQQP--PQQQPPP--PQQQPPPQQPHQPHQPHQPHQPHQPOQSSKP 137

Query Match 14.4%; Score 178; DB 4; Length 735;
Best Local Similarity 39.7%; Pred. No. 5e-06;
Matches 46; Conservative 6; Mismatches 40; Indels 24; Gaps 6;
Qy 157 PVAATPPAPPLHQPSPAAHAPP-----PPPGTTPPPASLPPPEAP 199
Db 138 VVAQGPSPAPGVSAPPASSAPPATPPTSGAAPPGGSPGPPTPTPPAVTSAPPAP 193

```


Db 464 VDSRRAARQASGPHEITITALVGAVTSLOOBLAHMRARTAPYGPYPPVGPYHPHADTE 523
 Qy 121 PAQPPRYPKAVVYLPPPHIAPPGRPLSLGAVPPPSYPPVAVTPGPAPPLHQPSDAAHAPP 180
 Db 524 PAQPPRYPKAVVYLPPPHIAPPGRPLSLGAVPPPSYPPVAVTPGPAPPLHQPSDAAHAPP 583
 Qy 181 PPPGPTPPDASLQPEAGAAGALVNASSAAHVNDTARAAD 224
 Db 584 PPPGPTPPDASLQPEAGAAGALVNASSAAHVNDTARAAD 627
 .
 RESULT 2
 US-10-214-932-86
 ; Sequence 86, Application US/10214932
 ; Publication No. US20030100707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HWANG, Irhwan
 ; APPLICANT: KIM, Dae Heon
 ; APPLICANT: LEE, Yong Jik
 ; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
 ; FILE REFERENCE: APB02/US
 ; CURRENT APPLICATION NUMBER: US/10/214,932
 ; CURRENT FILING DATE: 2002-08-08
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 86
 ; LENGTH: 635
 ; TYPE: PRT
 ; ORGANISM: Human herpesvirus 1.
 * US-10-214-932-86

Query Match 54.2%; Score 670.5; DB 14; Length 635;
 Best Local Similarity 63.4%; Pred No 9, 3e-36; Indels 7; Gaps 4;
 Matches 144; Conservative 12; Mismatches 6;
 Qy 1 AIAADROAGGLPAAAGDGGIRGSAKRRRHEVEQPEYDGRDDEPDRDFPPYGPBARPPEPR 60
 Db 403 AIAADROAGLQGQP-AAGDPVRGSGKRRYEAQPSSESYCDQEDADYYPGEARGAAGR 461
 Qy 61 VDSRRAARQASGPHEITITALVGAVTSLOOBLAHMRARTAPYGPYPPVGPYHPHADTE- 119
 Db 462 VDSRRAARQASGPHEITITALVGAVTSLOOBLAHMRARTAPYGPYPPVGPYHPHADTE- 521
 Qy 120 TPAQPPRYPKAVYLPPIAPPSSAA-YVPPPSYPPVAVTPGPAPLHQPSDAAH 177
 Db 522 TTHPALCPEATYRPPSSAPCQPGFASHAFTPPAACAQPGPFP--PCPSQT 578
 Qy 178 PPPPPGPTPPDASLQPEAGALVNASSAAHVNDTARAAD 224
 Db 579 RAPLPTEPAPATGSQPEASNAEGALVNASSAAHVNDTARAAD 625

RESULT 3
 US-10-425-115-315706
 ; Sequence 315706, Application US/10425115
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE: unsure
 ; NAME/KEY: unsure

Qy 1 LOCATION: (1)-(275)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_50997C.1.pep
 US-10-425-115-315706
 Query Match 17.9%; Score 222; DB 16; Length 275;
 Best Local Similarity 28.6%; Pred. No. 6, 3e-07;
 Matches 67; Conservative 10; Mismatches 83; Indels 74; Gaps 7;
 Qy 1 AIAADROAGGLPAAAGDGHCI-----RGSAKRRRHEVEQPEYDGR-----D 41
 Db 1 SLCPGRAGG---GGGRGFPRLALPQGDGAQRRLYDRLRRRFGRAGGLPRSQBPSD 57
 Qy 42 EPBD-----FYYPPGRAPRERPRVDSBRAAQASGHETITALVGAVTSLOOB 90
 Db 58 EPPREVKPTKTPPSXPTPHARSDTPXPFP-----87
 Qy 91 LAHMARTHA-PVGYPPVGPYHPHADTETPAQPRYPAKAVLPPPHIAPPSCPLSCA 149
 Db 88 -----HAPPPPPPLPPGPAPYXPYPPPPSPRPPSPRPPHPPPPSPSPXPFP 139
 Qy 150 VPPPSYPPVAVTPGPAPLHQPSDAAHPPSPRPPGPTPPAASLQPPAPGAEA 203
 Db 140 RPPP--PPGGPPPPAPXPXPPRPPAPRPPRPPPDPPPPPPPPXPPPPRA 191
 RESULT 4
 US-10-767-701-42767
 ; Sequence 42767, Application US/10767701
 ; Publication No. US2004012684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21 (5323)B
 ; CURRENT APPLICATION NUMBER: US/10/767 701
 ; CURRENT FILING DATE: 2004-01-29
 ; SEQ ID NO 42767
 ; SEQ ID NOS: 63128
 ; LENGTH: 376
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: SORBI-2BMAY03-C17099_1.pep
 US-10-767-701-42767

Query Match 17.9%; Score 221.5; DB 16; Length 376;
 Best Local Similarity 34.1%; Pred. No. 9, 1e-07;
 Matches 71; Conservative 4; Mismatches 54; Indels 79; Gaps 11;
 Qy 4 ADROAG-GIUPAAAGDGHGIRGSAKRRRHEVEQPEYDGRDDEPDRDFPPYGPGEARPEPRVD 62
 Db 16 APRPGPQIPASA---CRGPQRGRGPRGPP-----APPPPRBPG 52
 Qy 63 SRRAA--RQASGHETITALVGAVTSLOOBLAHMRARTAPYGPYPP--VGPYHPPA 116
 Db 53 GPPAAGPQRPAPGP-----84
 Qy 117 DTETPAQPRYPAKAVLPPPHIAPPGPPLSVAVTPGPAPLHQPSDAAH 176
 Db 85 ----PAPPPPP----PPPAPPAPPPPPPPPPPPPPPPPPAP----124
 Qy 177 HPPPPGPTPPDASLQPEAARGAEAG 204
 Db 125 -PPPPPPPPPPPPPPPPPPPPPPGGRPG 151
 RESULT 5
 US-10-437-963-112806
 ; Sequence 112806, Application US/10437963

Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Barzakov, Brad
 APPLICANT: Barzakov, Andrey A.
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 112806
 LENGTH: 342
 TYPE: PRT
 ORGANISM: *Oryza sativa*
 FEATURE: NAME/KEY: unsure
 LOCATION: (1)..(342)
 OTHER INFORMATION: unsure at all xaa locations
 FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_16656C.1.pep
 US-10-437-963-112806

Query Match 17.7%; Score 219.5; DB 16; Length 342;
 Best Local Similarity 28.9%; Pred. No. 1..e-06;
 Matches 70; Conservative 8; Nismatches 81; Indels 83; Gaps 10;
 Qy 12 PAAAGDGHGIRGSAKERRHEVEQPEYDCGRDEPDRDPYGEARBPVYDSDRARAQAS 71
 Db 11 PHRAG---RGNARSTDPAQPH---DPPPPHPXPQOPPTHTPDPAGGAPTRH 60
 Qy 72 GPHEITITALGAVTSIQLQELAHMRARTHAAPGYPPVGPTH----PHADTBT---120
 Db 61 TPOQHHTA-----PHKCKKCPTRPPTXPBPPPSHSPPPSLSPHPPPTPTP 108
 Qy 121 -----PAQPPRYPAKAVYLPPPHIAPPGPPLSGAVPPPSYPPVAVTPGPAPPYH 169
 Db 109 TTPTTHPTHPTPPAHPPRNPKHNPNTPTTPTTPTPPPP---PPSPPPP---HPPPPPPP 161
 Qy 170 QPSP--AHAHPPPP--GTPPPPA-----SLPQPE 197
 Db 162 SPTPPLTPRFPQPPPLSHTNPLSLSGPTTPPPXPRSKRPPAQINNPIDSULPRPP 221
 Qy 198 AP 199
 Db 222 PP 223

RESULT 6
 US-10-424-599-163337
 Sequence 163337, Application US/10424599
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 163337
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:

Search completed: July 27, 2005, 12:35:16
Job time : 156 Secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:44 ; Search time 41 Seconds

(without alignments)

16.386 Million cell updates/sec
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Minimum Match 1.00%

Maximum Match 1.00%

Listing First 1000 summaries

Issued Patents AA:*

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- 2: /cgn2_6/pcodata/1/iaa/5B_COMB_pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	75.0	50	3	US-09-246-860-9
2	36	75.0	50	4	US-09-735-605-9
3	36	75.0	79	3	US-08-905-223-493
4	35	72.9	58	4	US-10-127-611-5
5	35	72.9	91	4	US-09-248-706A-19847
6	35	72.9	748	2	US-08-997-080-154
7	35	72.9	748	2	US-08-997-36-154
8	35	72.9	748	3	US-09-895-855-154
9	35	72.9	748	3	US-09-324-542-154
10	34	72.9	748	4	US-09-305-446-154
11	35	72.9	754	3	US-09-005-180A-3
12	34	70.8	102	4	US-09-513-999C-6366
13	34	70.8	154	4	US-09-192A-311
14	34	70.8	300	4	US-09-134-000C-5791
15	34	70.8	699	4	US-09-252-991A-12077
16	34	70.8	717	4	US-09-543-68A-5706
17	34	70.8	762	4	US-09-107-532A-4275
18	34	70.8	2584	3	US-08-936-135-4
19	33	70.8	2588	3	US-08-946-135-2
20	33	68.8	81	4	US-09-107-532A-7025
21	33	68.8	364	4	US-09-252-991A-22552
22	33	68.8	401	4	US-09-248-798A-1914
23	33	68.8	635	1	US-07-332-855-2
24	33	68.8	635	4	US-08-176-320-2
25	33	68.8	726	4	US-09-189A-8750
26	33	68.8	1009	4	US-09-762-724-10
27	33	68.8	1017	4	US-09-762-724-12

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	75.0	79	3	US-08-905-223-493
3	36	75.0	79	3	US-08-905-223-493
4	35	72.9	58	4	US-10-127-611-5
5	35	72.9	91	4	US-09-248-706A-19847
6	35	72.9	748	2	US-08-997-080-154
7	35	72.9	748	3	US-09-895-855-154
8	35	72.9	748	3	US-09-324-542-154
9	35	72.9	748	4	US-09-305-446-154
10	34	70.8	754	3	US-09-005-180A-3
11	35	72.9	754	3	US-09-513-999C-6366
12	34	70.8	102	4	US-09-192A-311
13	34	70.8	154	4	US-09-134-000C-5791
14	34	70.8	300	4	US-09-252-991A-12077
15	34	70.8	699	4	US-09-252-991A-22552
16	34	70.8	717	4	US-09-543-68A-5706
17	34	70.8	762	4	US-09-107-532A-4275
18	34	70.8	2584	3	US-08-936-135-4
19	33	70.8	2588	3	US-08-946-135-2
20	33	68.8	81	4	US-09-107-532A-7025
21	33	68.8	364	4	US-09-252-991A-22552
22	33	68.8	401	4	US-09-248-798A-1914
23	33	68.8	635	1	US-07-332-855-2
24	33	68.8	635	4	US-08-176-320-2
25	33	68.8	726	4	US-09-189A-8750
26	33	68.8	1009	4	US-09-762-724-10
27	33	68.8	1017	4	US-09-762-724-12

Result No.	Score	Query Match	Length	DB ID	Description
1	36	75.0	50	3	US-09-246-860-9
2	36	75.0	79	3	US-08-905-223-493
3	36	75.0	79	3	US-08-905-223-493
4	35	72.9	58	4	US-10-127-611-5
5	35	72.9	91	4	US-09-248-706A-19847
6	35	72.9	748	2	US-08-997-080-154
7	35	72.9	748	3	US-09-895-855-154
8	35	72.9	748	3	US-09-324-542-154
9	35	72.9	748	4	US-09-305-446-154
10	34	70.8	754	3	US-09-005-180A-3
11	35	72.9	754	3	US-09-513-999C-6366
12	34	70.8	102	4	US-09-192A-311
13	34	70.8	154	4	US-09-134-000C-5791
14	34	70.8	300	4	US-09-252-991A-12077
15	34	70.8	699	4	US-09-252-991A-22552
16	34	70.8	717	4	US-09-543-68A-5706
17	34	70.8	762	4	US-09-107-532A-4275
18	34	70.8	2584	3	US-08-936-135-4
19	33	70.8	2588	3	US-08-946-135-2
20	33	68.8	81	4	US-09-107-532A-7025
21	33	68.8	364	4	US-09-252-991A-22552
22	33	68.8	401	4	US-09-248-798A-1914
23	33	68.8	635	1	US-07-332-855-2
24	33	68.8	635	4	US-08-176-320-2
25	33	68.8	726	4	US-09-189A-8750
26	33	68.8	1009	4	US-09-762-724-10
27	33	68.8	1017	4	US-09-762-724-12

Result No.	Score	Query Match	Length	DB ID	Description
1	36	75.0	50	3	US-09-246-860-9
2	36	75.0	79	3	US-08-905-223-493
3	36	75.0	79	3	US-08-905-223-493
4	35	72.9	58	4	US-10-127-611-5
5	35	72.9	91	4	US-09-248-706A-19847
6	35	72.9	748	2	US-08-997-080-154
7	35	72.9	748	3	US-09-895-855-154
8	35	72.9	748	3	US-09-324-542-154
9	35	72.9	748	4	US-09-305-446-154
10	34	70.8	754	3	US-09-005-180A-3
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15	34	70.8	699	4	US-09-252-991A-22552
16	34	70.8	717	4	US-09-543-68A-5706
17	34	70.8	762	4	US-09-107-532A-4275
18	34	70.8	2584	3	US-08-936-135-4
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21	33	68.8	364	4	US-09-252-991A-22552
22	33	68.8	401	4	US-09-248-798A-1914
23	33	68.8	635	1	US-07-332-855-2
24	33	68.8	635	4	US-08-176-320-2
25	33	68.8	726	4	US-09-189A-8750
26	33	68.8	1009	4	US-09-762-724-10
27	33	68.8	1017	4	US-09-762-724-12

Result No.	Score	Query Match	Length	DB ID	Description
1	36	75.0	50	3	US-09-246-860-9
2	36	75.0	79	3	US-08-905-223-493
3	36	75.0	79	3	US-08-905-223-493
4	35	72.9	58	4	US-10-127-611-5
5	35	72.9	91	4	US-09-248-706A-19847
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11	35	72.9	754	3	US-09-513-999C-6366
12	34	70.8	102	4	US-09-192A-311
13	34	70.8	154	4	US-09-134-000C-5791
14	34	70.8	300	4	US-09-252-991A-12077
15	34	70.8	699	4	US-09-252-991A-22552
16	34	70.8	717	4	US-09-543-68A-5706
17	34	70.8	762	4	US-09-107-532A-4275
18	34	70.8	2584	3	US-08-936-135-4
19	33	70.8	2588	3	US-08-946-135-2
20	33	68.8	81	4	US-09-107-532A-7025
21	33	68.8	364	4	US-09-252-991A-22552
22	33	68.8	401	4	US-09-248-798A-1914
23	33	68.8	635	1	US-07-332-855-2
24	33	68.8	635	4	US-08-176-320-2
25	33	68.8	726	4	US-09-189A-8750
26	33	68.8	1009	4	US-09-762-724-10
27	33	68.8	1017	4	US-09-762-724-12

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	75.0	79	3	US-08-905-223-493
3	36	75.0	79	3	US-08-905-223-493
4	35	72.9	58	4	US-10-127-611-5
5	35	72.9	91	4	US-09-248-706A-19847
6	35	72.9	748	2	US-08-997-080-154
7	35	72.9	748	3	US-09-895-855-154
8	35	72.9	748	3	US-09-324-542-154
9	35	72.9	748	4	US-09-305-446-154
10	34	70.8	754	3	US-09-005-180A-3
11	35	72.9	754	3	US-09-513-999C-6366
12	34	70.8	102	4	US-09-192A-311
13	34	70.8	154	4	US-09-134-000C-5791
14	34	70.8	300	4	US-09-252-991A-12077
15	34	70.8	699	4	US-09-252-991A-22552
16	34	70.8	717	4	US-09-543-68A-5706
17	34	70.8	762	4	US-09-107-532A-4275
18	34	70.8	2584	3	US-08-936-135-4
19	33	70.8	2588	3	US-08-946-135-2
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102	30	62.5	158	4	US-09-635-359B-29	Sequence 29, App1	4	US-09-252-991A-31080
103	30	62.5	179	4	US-09-615-192A-289	Sequence 289, App1	4	US-09-134-001C-5330
104	30	62.5	202	4	US-09-134-000C-3978	Sequence 3978, App1	4	US-09-134-000C-5375
105	30	62.5	223	4	US-09-248-796A-16638	Sequence 16638, A	4	US-09-252-991A-21999
106	30	62.5	223	4	US-09-328-3522-4358	Sequence 4358, App1	4	US-09-711-164-380
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117	30	62.5	363	1	US-08-458-023B-6	Sequence 6, App1	3	US-09-294-923-3
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135	30	62.5	769	4	US-09-949-016-10665	Sequence 10665, A	4	US-09-538-092-1154
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137	30	62.5	1437	4	US-09-949-116-10535	Sequence 10535, A	4	US-08-353-700-1
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139	29	60.4	61	4	US-09-107-532A-4643	Sequence 4643, App1	4	US-09-949-016-8246
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154	29	60.4	311	4	US-09-248-796A-17522	Sequence 17522, A	4	US-09-270-767-31878
155	29	60.4	311	4	US-09-270-767-48591	Sequence 12324, A	4	US-09-270-767-44313
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159	29	60.4	296	4	US-09-540-236-2650	Sequence 2650, App1	4	US-09-270-767-32176
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171	29	60.4	377	3	US-09-299-843-42	Sequence 42, App1	4	US-09-10-430-2650
172	29	60.4	377	3	US-09-088-337B-42	Sequence 42, App1	4	US-09-540-12974
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251	28	US-09-107-433-3412	Sequence 3412, App	Sequence 8, App1
252	28	US-09-902-540-16220	Sequence 16220, A	Sequence 8, App1
253	28	US-09-252-991A-25576	Sequence 25576, A	Sequence 12, App1
254	28	US-09-270-767-33544	Sequence 33544, A	Sequence 7055, Ap
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256	28	US-09-154-083-8	Sequence 8, App1	Sequence 16, App1
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583	955	US-08-853-102-4	Sequence 4, Appli	Sequence 33, Appli
584	965	US-09-853-102-4	Sequence 2, Appli	Sequence 9, Appli
585	971	US-09-489-039A-13026	Sequence 13026, A	Sequence 9, Appli
586	972	US-08-335-844A-24	Sequence 11, Appli	Sequence 4438, AP
587	972	US-08-559-451-11	Sequence 11, Appli	Sequence 6642, AP
588	977	US-09-348-352-4591	Sequence 4591, AP	Sequence 6716, AP
589	977	US-09-449-28A-4	Sequence 22, Appli	Sequence 15680, A
590	977	US-09-129-366-22	Sequence 22, Appli	Sequence 15, Appli
591	987	US-09-949-016-10265	Sequence 6133, AP	Sequence 622, AP
592	1002	US-09-762-277-3	Sequence 4, Appli	Sequence 16, Appli
593	1032	US-08-844A-24	Sequence 24, Appli	Sequence 19931, A
594	1044	US-09-115-954-2	Sequence 24, Appli	Sequence 440, APP
595	1063	US-09-335-844A-22	Sequence 22, Appli	Sequence 6716, AP
596	1081	US-09-529-366-22	Sequence 22, Appli	Sequence 5733, AP
597	1085	US-09-734-674-4	Sequence 4, Appli	Sequence 100, APP
598	1157	US-09-538-092-13238	Sequence 13238, AP	Sequence 100, APP
599	1225	US-09-115-954-2	Sequence 3637, AP	Sequence 100, APP
600	1236	US-09-883-134-4	Sequence 4, Appli	Sequence 100, APP
601	1239	US-09-343-267-19	Sequence 4267, AP	Sequence 44981, A
602	1475	US-09-538-092-11660	Sequence 1160, AP	Sequence 100, APP
603	1618	US-08-462-467B-4	Sequence 4, Appli	Sequence 100, APP
604	2089	US-09-492-501B-8	Sequence 8, Appli	Sequence 100, APP
610	2325	US-08-417-089-6	Sequence 6, Appli	Sequence 44981, A

685	118	4	US-09-543-681A-5800	Sequence 5800, App	4	US-09-543-681A-4245
686	119	1	US-07-824-853-1	Sequence 1, App	4	US-09-543-681A-7648
687	119	2	US-08-937-972-5	Sequence 5, App	4	US-09-134-001C-4116
688	126	4	US-09-248-796A-15590	Sequence 15590, A	2	US-09-134-001C-4116
689	132	4	US-09-732-210-1313	Sequence 1313, A	3	US-09-134-001C-4116
690	132	4	US-09-732-210-1314	Sequence 1314, A	3	US-09-134-001C-4116
691	133	4	US-09-270-167-57154	Sequence 57154, A	4	US-09-248-796A-18584
692	134	4	US-09-621-4031	Sequence 4031, A	4	US-09-248-796A-13115
693	138	4	US-09-902-540-10829	Sequence 10829, A	4	US-09-270-767-41787
694	139	4	US-09-328-352-7201	Sequence 7201, A	4	US-09-270-767-48332
695	142	4	US-09-328-352-5761	Sequence 5761, A	2	US-09-319-989-2
696	143	4	US-09-134-000C-4059	Sequence 4059, A	3	US-09-134-001C-3461
697	144	4	US-09-230-078A-6	Sequence 6, App	4	US-09-248-196A-16392
698	144	4	US-09-540-12977	Sequence 12977, A	4	US-09-252-991A-29257
699	145	4	US-09-270-767-72454	Sequence 4754, A	2	US-09-198-452A-555
700	146	4	US-09-270-767-32237	Sequence 32237, A	2	US-09-134-001C-4815
701	148	4	US-09-252-991A-18029	Sequence 18029, A	4	US-09-602-777A-158
702	151	4	US-09-902-540-10111	Sequence 10111, A	4	US-09-134-000C-6430
703	155	4	US-09-270-767-32485	Sequence 32485, A	4	US-09-270-767-60531
704	155	4	US-09-270-767-41702	Sequence 41702, A	4	US-09-270-767-60531
705	159	3	US-08-796-792-2	Sequence 2, App	2	US-09-270-767-60531
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714	170	3	US-08-858-207A-519	Sequence 519, App	2	US-09-134-001C-4815
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716	175	4	US-09-252-991A-11877	Sequence 11877, A	4	US-09-134-001C-4815
717	175	4	US-09-902-540-116269	Sequence 16769, A	2	US-09-134-001C-4815
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725	187	4	US-09-248-796A-26092	Sequence 26092, A	2	US-09-134-001C-4815
726	190	4	US-09-270-767-43995	Sequence 43995, A	4	US-09-134-001C-4815
727	191	4	US-09-248-796A-20248	Sequence 20248, A	4	US-09-134-001C-4815
728	194	4	US-09-248-796A-14593	Sequence 14593, A	4	US-09-134-001C-4815
729	194	2	US-08-833-1575-8	Sequence 8, App	2	US-09-134-001C-4815
730	199	2	US-08-831-1575-9	Sequence 9, App	2	US-09-134-001C-4815
731	199	4	US-09-710-1342	Sequence 1342, A	4	US-09-134-001C-4815
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755	226	4	US-09-270-767-53555	Sequence 53555, A	2	US-09-134-001C-4815
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831	26	54.2	US-09-583-110-3391	Sequence 3391, Ap	US-09-949-016-7709	Sequence 7709, Ap
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839	26	54.2	US-09-086-118-21	Sequence 21, Appli	US-09-976-400-10	Sequence 10, Appli
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842	26	54.2	US-07-828-700-8	Sequence 8, Appli	US-09-702-57-10	Sequence 10, Appli
843	26	54.2	US-09-360-779-2	Sequence 2, Appli	US-09-270-767-4139	Sequence 4519, A
844	26	54.2	US-09-435-335-2	Sequence 2, Appli	PCT-US96-08081-2	Sequence 2, Appli
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846	26	54.2	US-09-724-23-79	Sequence 79, Appli	5510466-4	Patent No. 5510466
847	26	54.2	US-09-214-631-5	Sequence 5, Appli	5510466-4	Patent No. 5510466
848	26	54.2	US-08-213-03-2	Sequence 2, Appli	5510466	Sequence 11, Appli
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852	26	54.2	US-08-299-667-6	Sequence 6, Appli	5510466	Sequence 11, Appli
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860	26	54.2	US-09-054-226B-4	Sequence 4, Appli	5510466	Sequence 11, Appli
861	26	54.2	US-08-981-190B-3	Sequence 3, Appli	5510466	Sequence 11, Appli
862	26	54.2	US-09-134-001C-558B	Sequence 558B, Ap	5510466	Sequence 11, Appli
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878	26	54.2	US-09-020-540-12860	Sequence 3, Appli	5510466	Sequence 11, Appli
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882	26	54.2	US-09-052-991A-21686	Sequence 21686, A	5510466	Sequence 11, Appli
883	26	54.2	US-09-089-411A-7	Sequence 6647, Ap	5510466	Sequence 11, Appli
884	26	54.2	US-09-091-220A-14	Sequence 14, Appli	5510466	Sequence 11, Appli
885	26	54.2	US-09-252-991A-17143	Sequence 45205, A	5510466	Sequence 11, Appli
886	26	54.2	US-09-043-545-2	Sequence 2, Appli	5510466	Sequence 11, Appli
887	26	54.2	US-09-080-404-381-2	Sequence 10, Appli	5510466	Sequence 11, Appli
888	26	54.2	US-09-080-404-381-2	Sequence 10569, A	5510466	Sequence 11, Appli
889	26	54.2	US-09-089-462-467B-10	Sequence 16038, A	5510466	Sequence 11, Appli
890	26	54.2	US-09-089-462-467B-10	Sequence 17003, A	5510466	Sequence 11, Appli
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893	26	54.2	US-09-089-462-467B-10	Sequence 4879, Ap	5510466	Sequence 11, Appli
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898	26	54.2	US-09-089-462-467B-10	Sequence 4879, Ap	5510466	Sequence 11, Appli
899	26	54.2	US-09-089-462-467B-10	Sequence 4879, Ap	5510466	Sequence 11, Appli
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902	26	54.2	US-09-089-462-467B-10	Sequence 4879, Ap	5510466	Sequence 11, Appli
903	26	54.2	US-09-089-462-467B-10	Sequence 4879, Ap	5510466	Sequence 11, Appli

RESULT 4
US-10-127-641-5
Sequence 5, Application US/10127641
GENERAL INFORMATION:
APPLICANT: Hart, Mary Kate
TITLE OF INVENTION: Prophylactic and Therapeutic Monoclonal Antibodies
FILE REFERENCE: 003/251/SAP
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: US 60/285,601
PRIOR FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 5
SEQ ID NO: 5
SOFTWARE: Apple Macintosh Microsoft Word 6.0
LENGTH: 58
TYPE: PRT
ORGANISM: Eastern equine encephalitis virus
US-10-127-641-5

Query Match 72.9%; Score 35; DB 4; Length 58;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 30 PHETITLML 37

RESULT 5
US-09-248-796A-19847
Sequence 19847, Application US/09248796A
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO: 19847
LENGTH: 91
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19847

Query Match 72.9%; Score 35; DB 4; Length 91;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 62 PHEYITAL 69

RESULT 6
US-08-997-080-154
Sequence 154, Application US/08997080
GENERAL INFORMATION:
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman

RESULT 7
US-08-997-362-154
Sequence 154, Application US/08997362
GENERAL INFORMATION:
APPLICANT: TAN, Paul
APPLICANT: Hiwama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestridge, Rosalie
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

RESULT 8
US-08-997-080-154
Sequence 154, Application US/08997080
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873, 970
 FILING DATE: June 12, 1997
 APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705, 347
 FILING DATE: August 29, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sleath, Janet
 REGISTRATION NUMBER: 37, 007
 REFERENCE/DOCKET NUMBER: 11000.1002c2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-269-0565
 TELEX: 206-269-0563
 INFORMATION FOR SEQ ID NO: 154:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 748 amino acids
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLOGY: linear
 US-08-987-362-154

Query Match 72.9%; Score 35; DB 2; Length 748;
 Best Local Similarity 77.8%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHEITAL 9
 Db 405 GPHEITAL 413

RESULT 9
 US-09-324-542-154
 Sequence 154, Application US/09324542
 GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 PATENT NO. 6328978
 APPLICANT: Tan, Paul L.J.
 APPLICANT: Prestidge, Ross
 TITLE OF INVENTION: Methods and Compounds for the Treatment
 of Immunologically-Mediated Skin Disorders
 FILE REFERENCE: 11000.1007c1
 CURRENT APPLICATION NUMBER: US/09/324, 542
 EARLIER FILING DATE: 1999-06-02
 EARLIER APPLICATION NUMBER: US 08/997, 080
 EARLIER FILING DATE: 1997-12-23
 NUMBER OF SEQ ID NOS: 194
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 154
 LENGTH: 748
 TYPE: PRT
 ORGANISM: Mycobacterium vaccae
 FEATURE:
 NAME/KEY: JNSURE
 LOCATION: (119) ... (119)

Query Match 72.9%; Score 35; DB 3; Length 748;
 Best Local Similarity 77.8%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHEITAL 9
 Db 405 GPHEITAL 413

RESULT 10
 US-09-095-855-154
 Sequence 154, Application US/09095855
 GENERAL INFORMATION:
 APPLICANT: Tan, Paul
 PATENT NO. 6160093
 APPLICANT: Visser, Elizabeth
 APPLICANT: Skinner, Margot
 APPLICANT: Prestidge, Ross
 TITLE OF INVENTION: Compounds and Methods for
 Treatment and Diagnosis of Mycobacterial Infections
 TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
 NUMBER OF SEQUENCES: 208
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Ann W. Speckman
 STREET: 2601 Elliott Avenue, Suite 4185
 CITY: Seattle
 STATE: WA
 ZIP: 98121
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/095, 855
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/705, 347
 FILING DATE: 29-AUG-1996
 APPLICATION NUMBER: 0/873, 970
 FILING DATE: 12-JUN-1997
 APPLICATION NUMBER: 08/997, 362
 FILING DATE: 23-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Sleath, Janet
 REGISTRATION NUMBER: 37, 007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-269-0565
 TELEX:
 INFORMATION FOR SEQ ID NO: 154:

SEQ ID NO 154
 LENGTH: 748
 TYPE: PRT
 ORGANISM: Mycobacterium vaccae
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (119)...(119)
 US-09-205-426-154

RESULT 12
 LENGTH: 748
 Best Local Similarity 72.9%; Score 35; DB 4; Length 748;
 Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 Query 1 GPHEITAL 9
 Db 405 GPHEITRAL 413

RESULT 11
 US-09-005-180A-3
 Sequence 3, Application US/09005180A
 Patent No. 6124446
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: HUMAN VPS35/MEM3-RELATED PROTEIN
 NUMBER OF SEQUENCES: 4
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,180A
 FILING DATE: Filed January 8, 1998
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REFERENCE/DOCKET NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0457 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-845-4166
 TELEFAX: 650-855-0555
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 754 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 1354049
 US-09-005-180A-3

Query Match 2 PHETITAL 9
 Best Local Similarity 75.0%; Score 35; DB 3; Length 754;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Query 2 PHETITAL 9
 Db 523 PHOTISAL 530

RESULT 13
 US-09-615-192A-311
 Sequence 311, Application US/09615192A
 Patent No. 6110718
 GENERAL INFORMATION:
 APPLICANT: Blokberg, Leonard N.
 APPLICANT: Havukkala, Ilkka
 TITLE OF INVENTION: Materials and Methods for the
 FILE REFERENCE: 11000-1003c4U
 CURRENT APPLICATION NUMBER: US/09/615,192A
 PRIOR APPLICATION NUMBER: US 08/975,316
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: US 08/713,000
 PRIOR FILING DATE: 1996-09-11
 PRIOR APPLICATION NUMBER: US 09/169,789
 PRIOR FILING DATE: 1998-10-09
 NUMBER OF SEQ ID NOS: 405
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 311
 LENGTH: 154
 TYPE: PRT

RESULT 14
 ORGANISM: *Pinus radiata*
 SEQ ID NO: 615-192A-311
 Query Match Similarity 70.8%; Score 34; DB 4; Length 154;
 Best Local Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PHETITAL 9
 Db 611 PHQAITAL 68

RESULT 14
 Sequence 5791, Application US/09134000C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 FILE REFERENCE: 032/296-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 5791
 TYPE: PRT
 ORGANISM: *Enterococcus faecalis*
 US-09-134-000C-5791

Query Match Similarity 70.8%; Score 34; DB 4; Length 300;
 Best Local Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PHETITAL 9
 Db 28 PHQITL 35

RESULT 15
 Sequence 17077, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 TITLE OF INVENTION: *AERGINOSA* FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 17077
 LENGTH: 699
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-17077

Query Match Similarity 70.8%; Score 34; DB 4; Length 699;
 Best Local Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GPHEITAL 9
 Db 347 GPHQPIVAL 355

RESULT 16
 US-09-543-681A-5706
 Sequence 5706, Application US/09543681A
 Patent No. 6605709
 GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PROTEUS MIRABILIS*
 FILE REFERENCE: 2709 1002-001
 CURRENT APPLICATION NUMBER: US/09/543,681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO 5706
 LENGTH: 717
 TYPE: PRT
 ORGANISM: *Proteus mirabilis*
 US-09-543-681A-5706

Query Match Similarity 70.8%; Score 34; DB 4; Length 717;
 Best Local Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GPHEITAL 9
 Db 497 GPHETITAL 505

RESULT 17
 US-09-107-532A-4275
 Sequence 4275, Application US/09107532A
 Patent No. 6581275
 GENERAL INFORMATION:
 APPLICANT: Lynn A. Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESS: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM IS09660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Danake
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4275:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 762 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium
 FEATURE: misc feature
 LOCATION: (B) LOCATION 1...762
 SEQ ID NO: 4275:
 US-09-107-532A-4275

Query Match Score 34; DB 4; Length 762;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GPHEITAL 9
 Db 383 GPHELNSL 391

RESULT 18
 US-08-936-135-4
 Sequence 4, Application US/08936135
 Patent No. 6054293
 GENERAL INFORMATION:
 APPLICANT: Tessier-Lavigne, Marc
 APPLICANT: He, Zhigang
 APPLICANT: Chen, Hang
 TITLE OF INVENTION: Semaphorin Receptors
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/936,135
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UC97-288-2
 TELECOMMUNICATION: (650) 343-4341
 TELEFAX: (650) 343-4442
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2588 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 US-08-936-135-2

Query Match Score 34; DB 3; Length 2588;
 Best Local Similarity 66.7%; Pred. No. 6.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GPHEITAL 9
 Db 1167 GPHEGLVAL 1175

RESULT 20
 US-09-107-532A-7025
 Sequence 7025, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 PRIORITY APPLICATION NUMBER: 60/08936135
 GENERAL INFORMATION:
 APPLICANT: Tessier-Lavigne, Marc

RESULT 19
 US-08-936-135-2
 Sequence 2, Application US/08936135
 Patent No. 6054293
 GENERAL INFORMATION:
 APPLICANT: Tessier-Lavigne, Marc

FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Aminello, Pamela Denene
 REGISTRATION NUMBER: 40,489
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-5277
 INFORMATION FOR SEQ ID NO: 7025:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 81 amino acids
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..81
 SEQUENCE DESCRIPTION: SEQ ID NO: 7025:
 US-09-107-53A-7025:
 Query Match 68.8%; Score 33; DB 4; Length 81;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 21
 US-09-252-991A-22252
 Sequence 22552, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenstein et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 22552
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-22252:
 Query Match 68.8%; Score 33; DB 4; Length 364;
 Best Local Similarity 75.0%; Pred. No. 1e-02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 RESULT 22
 US-09-248-796A-19514
 Sequence 19514, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 10:196..132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 19514
 LENGTH: 401
 TYPE: PRT
 ORGANISM: Candida albicans
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (87)
 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
 US-09-248-796A-19514:
 Query Match 68.8%; Score 33; DB 4; Length 401;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PHETITAL 9
 Db 114 PHSTISAL 121
 RESULT 23
 US-07-832-855-2
 Sequence 2, Application US/07832855
 Patent No. 5478727
 GENERAL INFORMATION:
 APPLICANT: Roizman, Bernard
 APPLICANT: Liu, Fenyong
 TITLE OF INVENTION: Methods and Compositions of a
 TITLE OF INVENTION: Preparation and Use of A Herpes Protease
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD, WHITE & DURKEE
 STREET: 321 No. 5478727th Clark Street, Suite 800
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/832,855
 FILING DATE: 1992-07-07
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Cooley, Ronald B.
 REGISTRATION NUMBER: 27,187
 REFERENCE/DOCKET NUMBER: ARCD045
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (312) 245-4961
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 635 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-832-855-2:
 Query Match 68.8%; Score 33; DB 1; Length 635;
 Best Local Similarity 77.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GPHEITTA 8
 Db 31 GPRTSTA 38
 RESULT 24
 US-09-248-796A-19514
 Sequence 19514, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 10:196..132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 Qy 1 GPHEITTA 9
 Db 473 GTNETITTA 481

RESULT 24

US-08-176-320-2

Sequence 2, Application US/08176320

Patent No. 6410704

GENERAL INFORMATION:

APPLICANT: Roizman, Bernard

APPLICANT: Liu, Fenyong

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREPARATION AND USE OF A HERPES PROTEASE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Alice O. Martin

STREET: 321 No. 6410704th Clark Street, Suite 800

CITY: Chicago

STATE: ILL

COUNTRY: USA

ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,320

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/705,814

FILING DATE: 24-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cooley, Ronald B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)744-0090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

LENGTH: 635 amino acids

STRANDEDNESS: single

TOPOLOGY: linear

US-08-176-320-2

Query Match Score 68.8%; Pred. No. 2e+02; Length 635;

Best Local Similarity 77.8%; Mismatches 1; Indels 0; Gaps 0;

Matches 7;

Qy 1 GPHETITAL 9

Db 473 GTNETITAL 481

RESULT 25

US-09-489-039A-8750

Sequence 8750, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709.2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 09/489,039A

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8750

LENGTH: 726

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8750

Query Match Score 68.8%; Pred. No. 3.4e+02; Length 726;

Best Local Similarity 83.3%; Mismatches 1; Indels 0; Gaps 0;

Matches 5;

Qy 2 PHETIT 7

Db 912 PHETVT 917

RESULT 26

US-09-762-724-10

Sequence 10, Application US/09762724

Patent No. 6664053

GENERAL INFORMATION:

APPLICANT: Kovacs, et al.

TITLE OF INVENTION: Identification of a region of the major surface glycoprotein (MSG) gene of human *Pneumocystis carinii*

FILE REFERENCE: 4239-58054

CURRENT APPLICATION NUMBER: US/09/762,724

PRIOR APPLICATION NUMBER: PCT/US99/18750

PRIOR FILING DATE: 1999-08-17

PRIOR APPLICATION NUMBER: US 60/096,805

PRIOR FILING DATE: 1998-08-17

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 1009

TYPE: PRT

ORGANISM: *Pneumocystis carinii* sp. f. hominis

US-09-762-724-10

Query Match Score 68.8%; Pred. No. 3.4e+02; Length 1009;

Best Local Similarity 83.3%; Mismatches 1; Indels 0; Gaps 0;

Matches 5;

Qy 2 PHETIT 7

Db 921 PHETVT 926

RESULT 27

US-09-762-724-12

Sequence 12, Application US/09762724

Patent No. 6664053

GENERAL INFORMATION:

APPLICANT: Kovacs, et al.

TITLE OF INVENTION: Identification of a region of the major surface glycoprotein (MSG) gene of human *Pneumocystis carinii*

FILE REFERENCE: 4239-58054

CURRENT APPLICATION NUMBER: US/09/762,724

PRIOR APPLICATION NUMBER: PCT/US99/18750

PRIOR FILING DATE: 1999-08-17

PRIOR APPLICATION NUMBER: US 60/096,805

PRIOR FILING DATE: 1998-08-17

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 1017

TYPE: PRT

ORGANISM: *Pneumocystis carinii* sp. f. hominis

US-09-762-724-12

Query Match Score 68.8%; Pred. No. 3.4e+02; Length 1017;

Best Local Similarity 83.3%; Mismatches 1; Indels 0; Gaps 0;

Matches 5;

Qy 2 PHETIT 7

Db 912 PHETVT 917

RESULT 28

US-09-762-724-14
 / Sequence 14, Application US/09762724
 / Patent No. 6664053
 / GENERAL INFORMATION:
 / APPLICANT: Kovacs, et al.
 / TITLE OF INVENTION: Identification of a region of the major surface
 / TITLE INVENTION: Glycoprotein (MSG) gene of human Pneumocystis carinii
 / CURRENT APPLICATION NUMBER: US/09/762,724
 / CURRENT FILING DATE: 2001-02-09
 / PRIOR APPLICATION NUMBER: PCT/US99/18750
 / PRIOR FILING DATE: 1999-08-17
 / PRIOR APPLICATION NUMBER: US 6,0/096,805
 / PRIOR FILING DATE: 1998-08-17
 / NUMBER OF SEQ ID NOS: 26
 / SEQ ID NO 14
 / SOFTWARE: PatentIn Ver. 2.0
 / LENGTH: 1023
 / TYPE: PRT
 / ORGANISM: Pneumocystis carinii sp. f. hominis
 / US-09-762-724-14

Query Match 68.8%; Score 33; DB 4; Length 1023;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
 Db 916 PHETVT 921

RESULT 29
 US-09-762-724-8
 / Sequence 8, Application US/09762724
 / Patent No. 6664053
 / GENERAL INFORMATION:
 / APPLICANT: Kovacs, et al.
 / TITLE OF INVENTION: Identification of a region of the major surface
 / TITLE INVENTION: Glycoprotein (MSG) gene of human Pneumocystis carinii
 / CURRENT APPLICATION NUMBER: US/09/762,724
 / CURRENT FILING DATE: 2001-02-09
 / PRIOR APPLICATION NUMBER: PCT/US99/18750
 / PRIOR FILING DATE: 1999-08-17
 / NUMBER OF SEQ ID NOS: 26
 / SEQ ID NO 8
 / SOFTWARE: PatentIn Ver. 2.0
 / LENGTH: 1027
 / TYPE: PRT
 / ORGANISM: Pneumocystis carinii sp. f. hominis
 / US-09-762-724-8

Query Match 68.8%; Score 33; DB 4; Length 1027;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
 Db 922 PHETVT 927

RESULT 30
 US-09-513-999C-5317
 / Sequence 5317, Application US/09513999C
 / Patent No. 6783961
 / GENERAL INFORMATION:
 / APPLICANT: Dumas Milne Edwards, J.B.
 / APPLICANT: Duclert, A.
 / APPLICANT: Giordano, J.Y.
 / TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 / Patent No. 6783961

FILE REFERENCE: 59.US2.REG
 / CURRENT APPLICATION NUMBER: US/09/513,999C
 / CURRENT FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: US 60/122,487
 / PRIOR FILING DATE: 1999-02-26
 / NUMBER OF SEQ ID NOS: 36681
 / SOFTWARE: Patent.pm
 / SEQ ID NO 5317
 / LENGTH: 108
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: UNSURE
 / LOCATION: 46
 / OTHER INFORMATION: Xaa=Glu or Gly
 / FEATURE:
 / NAME/KEY: UNSURE
 / LOCATION: 48
 / OTHER INFORMATION: Xaa=Lys or Asn
 / FEATURE:
 / NAME/KEY: UNSURE
 / LOCATION: 55
 / OTHER INFORMATION: Xaa=Asp or Glu
 / FEATURE:
 / NAME/KEY: UNSURE
 / LOCATION: 88
 / OTHER INFORMATION: Xaa=Ile or Met
 / FEATURE:
 / NAME/KEY: UNSURE
 / LOCATION: 91
 / OTHER INFORMATION: Xaa=Ala or Pro
 / US-09-513-999C-5317

Query Match 66.7%; Score 32; DB 4; Length 108;
 Best Local Similarity 85.7%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPHEIT 7
 Db 96 GPEETIT 102

RESULT 31
 US-09-007-484-4
 / Sequence 4, Application US/09007484
 / Patent No. 6072032
 / GENERAL INFORMATION:
 / APPLICANT: Black, Michael T.
 / TITLE OF INVENTION: No. 6072032el Ftsy
 / NUMBER OF SEQUENCES: 4
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Dechert Price & Rhoads
 / CITY: Philadelphia
 / STATE: PA
 / ZIP: 19103
 / COUNTRY: US
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FASSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/007,484
 / FILING DATE:
 / CLASSIFICATION:
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Falk, Stephen T.
 / REGISTRATION NUMBER: 36,795
 / REFERENCE/DOCKET NUMBER: GM10081

TELECOMMUNICATION INFORMATION:
 TELEFAX: 215-994-2222
 TELEX: 215-994-2222
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 277 amino acids
 TYPE: amino acid
 STRANDBEDNESS: single
 TOPOLOGY: linear
 us-09-007-484-4

Query Match 66.7%; Score 32; DB 3; Length 277;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
 Db 192 PHETFL 199

RESULT 32
 US-09-309-682-4
 Sequence 4, Application US/09309682
 Patent No. 6214348
 GENERAL INFORMATION:
 APPLICANT: Black, Michael T.
 TITLE OF INVENTION: NO. 6214348e1 Ft&BY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechart Price & Rhoads
 STREET: 4000 Bell Atlantic Tower, 1717 Arch Stree
 CITY: Philadelphia
 STATE: PA
 COUNTRY: US
 ZIP: 19103
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/309,682
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/007,484
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Falk, Stephen T.
 REGISTRATION NUMBER: 36,795
 REFERENCE/DOCKET NUMBER: GM10081
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-994-2488
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 277 amino acids
 TYPE: amino acid
 STRANDBEDNESS: single
 TOPOLOGY: linear
 us-09-309-682-4

Query Match 66.7%; Score 32; DB 3; Length 277;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
 Db 192 PHETFL 199

RESULT 33
 US-09-335-409-22
 Sequence 22, Application US/09335409
 Patent No. 6121029
 GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligorn, James
 APPLICANT: Molnar, Istvan
 APPLICANT: Zirkle, Ross
 APPLICANT: Cyr, Devon
 APPLICANT: Goerlach, Joern
 TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 FILE REFERENCE: 4-30582A
 CURRENT APPLICATION NUMBER: US/09/335,409
 CURRENT FILING DATE: 1999-06-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 305
 TYPE: PRT
 ORGANISM: Sorangium cellulosum
 US-09-335-409-22

Query Match 66.7%; Score 32; DB 3; Length 305;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHEITITAL 9
 Db 250 GPHEVLVVL 258

RESULT 34
 US-09-568-102-22
 Sequence 22, Application US/09568102
 Patent No. 6346404
 GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligorn, James
 APPLICANT: Molnar, Istvan
 APPLICANT: Zirkle, Ross
 APPLICANT: Cyr, Devon
 APPLICANT: Goerlach, Joern
 TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 FILE REFERENCE: 4-30582A
 CURRENT APPLICATION NUMBER: US/09/568,102
 CURRENT FILING DATE: 2000-05-10
 PRIOR APPLICATION NUMBER: 09/335,409
 PRIOR FILING DATE: 1999-06-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 305
 TYPE: PRT
 ORGANISM: Sorangium cellulosum
 US-09-568-102-22

Query Match 66.7%; Score 32; DB 3; Length 305;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHEITITAL 9
 Db 250 GPHEVLVVL 258

RESULT 35
 US-09-567-969-22
 Sequence 22, Application US/09567969
 Patent No. 6355457
 GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligorn, James

APPLICANT: Molnar, Istvan
 APPLICANT: Zirkle, Ross
 APPLICANT: Cyr, Devon
 APPLICANT: Goerlach, Joern
 TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 CURRENT APPLICATION NUMBER: US/09/567,969
 CURRENT FILING DATE: 2000-05-10
 PRIORITY APPLICATION NUMBER: 09/335,409
 PRIORITY FILING DATE: 1999-06-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 305
 TYPE: PRT
 ORGANISM: Sorangium celluloseum
 US-09-567-969-22

Query Match 66.7%; Score 32; DB 3; Length 305;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHEITAL 9
 Db 250 GPHEVLVVL 258

RESULT 36
 US-09-568-480-22
 Sequence 22, Application US/09568480
 Patent No. 6355458
 GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligon, James
 APPLICANT: Molnar, Istvan
 APPLICANT: Zirkle, Ross
 APPLICANT: Cyr, Devon
 APPLICANT: Goerlach, Joern
 TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 FILE REFERENCE: 4-30582A
 CURRENT FILING DATE: 2000-05-10
 PRIORITY APPLICATION NUMBER: 09/335,409
 PRIORITY FILING DATE: 1999-06-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 305
 TYPE: PRT
 ORGANISM: Sorangium celluloseum
 US-09-568-480-22

Query Match 66.7%; Score 32; DB 3; Length 305;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHEITAL 9
 Db 250 GPHEVLVVL 258

RESULT 37
 US-09-568-486-22
 Sequence 22, Application US/09568486
 GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligon, James
 APPLICANT: Molnar, Istvan
 APPLICANT: Zirkle, Ross
 APPLICANT: Cyr, Devon
 APPLICANT: Goerlach, Joern
 TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 FILE REFERENCE: 4-30582A
 CURRENT FILING DATE: 2000-05-10
 PRIORITY APPLICATION NUMBER: 09/335,409
 PRIORITY FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 22
 LENGTH: 305
 TYPE: PRT
 ORGANISM: Sorangium cellulosum
 US-09-567-899-22

Query Match 66.7%; Score 32; DB 3; Length 305;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 SEQ ID NO: 4994

Qy 1 GPHETITAL 9
 Db 250 GPHEVLYNL 258

RESULT 40
 US-09-328-352-4994
 Sequence 4994, Application US/09328352
 Patent No. 6562988

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO: 4994
 LENGTH: 307
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-4994

Query Match 66.7%; Score 32; DB 4; Length 307;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 4994

Qy 1 GPHETIT 7
 Db 124 GPHLTIT 130

RESULT 41
 US-09-902-540-11852
 Sequence 11852, Application US/09902540
 Patent No. 6833447

GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-1011549
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO: 11852
 LENGTH: 315
 TYPE: PRT
 ORGANISM: Myxococcus xanthus
 US-09-902-540-11852

Query Match 66.7%; Score 32; DB 4; Length 315;
 Best Local Similarity 62.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
 Db 35 PHETVEAV 42

RESULT 42
 US-09-489-039A-12482
 Sequence 12482, Application US/09489039A
 Patent No. 6610436

GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709 2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO: 12482
 LENGTH: 383
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12482

Query Match 66.7%; Score 32; DB 4; Length 383;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
 Db 276 GVHETITBL 284

RESULT 43
 US-08-986-963-2
 Sequence 2, Application US/08986963
 Patent No. 5958730

GENERAL INFORMATION:
 APPLICANT: Rosateck Jr., Paul R.
 TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
 TITLE OF INVENTION: PTIV
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: US
 ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/986,963
 FILING DATE: December 8, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Webster, Thomas D.
 REGISTRATION NUMBER: 39,872
 REFERENCE/DOCKET NUMBER: X-11763
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317/276-3334
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-986-963-2

Query Match 66.7%; Score 32; DB 2; Length 425;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHETITAL 9 ; INFORMATION FOR SEQ ID NO: 2:
 Db 340 PHETFLAL 347 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 430 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-09-007-484-2

RESULT 44
 US-09-583-110-4561
 Sequence 4561, Application US/09583110
 Patent No. 6699703
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 FILE REFERENCE: PATH00-07A
 CURRENT APPLICATION NUMBER: US/09/583,110
 PRIOR APPLICATION NUMBER: US 09/107,433
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/085,131
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: US 60/051,553
 PRIOR FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO 4561
 TYPE: PRT
 ORGANISM: Streptococcus pneumoniae
 US-09-583-110-4561

Query Match 66.7%; Score 32; DB 4; Length 429;
 Best Local Similarity 75.0%; Prod. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHETITAL 9 ; INFORMATION FOR SEQ ID NO: 2:
 Db 344 PHETFLAL 351 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 430 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-09-007-484-2

RESULT 46
 US-09-109-682-2
 Sequence 2, Application US/09309682
 Patent No. 6214348
 GENERAL INFORMATION:
 APPLICANT: Black, Michael T.
 TITLE OF INVENTION: No. 6214348el FtsY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 400 Bell Atlantic Tower, 1717 Arch Stree
 CITY: Philadelphia
 STATE: PA
 COUNTRY: US
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/309,682
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/007,484
 ATTORNEY/AGENT INFORMATION:
 NAME: Falk, Stephen T
 REGISTRATION NUMBER: 36,795
 REFERENCE/DOCKET NUMBER: GM1.0081
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-994-2438
 TELEFAX: 215-994-2222
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 Sequence 2, Application US/09007484
 Patent No. 6072032
 GENERAL INFORMATION:
 APPLICANT: Black, Michael T.
 TITLE OF INVENTION: No. 6072032el FtsY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 400 Bell Atlantic Tower, 1717 Arch Stree
 CITY: Philadelphia
 STATE: PA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/007,484
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Falk, Stephen T
 REGISTRATION NUMBER: 36,795
 REFERENCE/DOCKET NUMBER: GM1.0081
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-994-2488
 TELEFAX: 215-994-2222
 RESULT 47
 US-09-107-433-2686
 Sequence 2686, Application US/09107433

Patent No. 6800744
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID
 SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS
 NUMBER OF SEQUENCES: 5206
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 110 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 024354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinieillo, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-8007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 2686:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 430 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pneumoniae
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...430
 SEQUENCE DESCRIPTION: SEQ ID NO: 2686:
 US-09-107,433-2686

Query Match 66.7%; Score 32; DB 4; Length 430;
 Best Local Similarity 75.0%; Pred. No. 2e+02; Indels 0; Gaps 0;

RESULT 48
 US-09-540-236-2280
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 PATENT NO. 6673910
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAF
 FILE REFERENCE: 2739.2005-001
 CURRENT APPLICATION NUMBER: US/09/540,236
 CURRENT FILING DATE: 2000-04-04
 NUMBER OF SEQ ID NOS: 3840
 SEQ ID NO 2280
 LENGTH: 431
 TYPE: PRT

; ORGANISM: M.catarrhalis
 US-09-540-236-2280
 Query Match 66.7%; Score 32; DB 4; Length 431;
 Best Local Similarity 66.7%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GPHTTIAL 9
 Db 179 GEHQITAL 187

RESULT 49
 US-09-413-814-72
 Sequence 72, Application US/09413814
 Patent No. 6225054
 GENERAL INFORMATION:
 APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 APPLICANT: Brisol-Myers Squibb, Co.
 APPLICANT: Beyer, Stefan
 APPLICANT: Bloecker, Helmut
 APPLICANT: Brandt, Petra
 APPLICANT: Cino, Paul M
 APPLICANT: Dougherty, Brian A
 APPLICANT: Goldberg, Steven L
 APPLICANT: Hofle, Gerhard
 APPLICANT: Mueller, Joachim
 APPLICANT: Reichenbach, Hans
 TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or heteropolyketide compounds
 TITLE OF INVENTION: heteropolyketide compounds
 FILE REFERENCE: PCT/US 99/23535
 CURRENT APPLICATION NUMBER: US/09/413,814
 CURRENT FILING DATE: 1999-10-07
 EARLIER APPLICATION NUMBER: DB 198 46 493.2
 EARLIER FILING DATE: 1998-10-09
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 72
 LENGTH: 492
 TYPE: PRT
 ORGANISM: Sorangium cellulosum
 US-09-413-814-72

Query Match 66.7%; Score 32; DB 3; Length 492;
 Best Local Similarity 55.6%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GPHTTIAL 9
 Db 437 GPHEVVLV 445

RESULT 50
 US-09-328-352-7300
 Sequence 7300, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 7300
 LENGTH: 536
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-7300

Query Match 66.7%; Score 32; DB 4; Length 536;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
| : |||||
Db 285 GEHOITAL 293

Search completed: July 27, 2005, 12:42:50
Job time : 53 secs